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AAY92237 AAB31682 AAO20555 ABG96366

ABG73169 ABR47522 ADC78795 ABP01586 ABB63376

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Copyright (c) 1993 - 2004 Compugen Ltd.   September 11, 2004, 21:23:37; Search time 94 Seconds (without alignments) 24:047 Million cell updates/seconds (without alignments) 24:047 Million cell updates/seconds (without alignments) 24:047 Million cell updates/seconds (apport 0.0; dapext 0.5 1586107 seqs, 282547505 residues	25 100.0 25 100.0 25 100.0	25 100.0 25 100.0 25 100.0	25 100.0 25 100.0 25 100.0	25 100.0 25 100.0 25 100.0	25 100.0 25 100.0 25 100.0	25 100.0 25 100.0	25 100.0 25 100.0	25 100.0 25 100.0 25 100.0	25 100.0 25 100.0 25 100.0	25 100.0 899 25 100.0 90	25 100.0 25 100.0 25 100.0	25 100.0 95 25 100.0 95 25 100.0 95	64 25 100.0 95 5 65 25 100.0 95 5 66 25 100.0 95 5 67 25 100.0 95 6	25 100.0 95 25 100.0 95 25 100.0 97	25 100.0 98	25 100.0 99 25 100.0 101 25 100.0 101	25 100.0 105 25 100.0 105	25 100.0 106	25 100.0 108	25 100.0 109 25 100.0 110	25 100.0 110	25 100.0 114 25 100.0 114 25 100.0	25 100.0 116 25 100.0 116	25 100.0 120 25 100.0 121	25 100.0 123 25 100.0 124	25 100.0 125	25 100.0 125 25 100.0 126
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diabetes; Cushing's disease; eating disorder; AIDS; growth hormone deficiency.

/note= "Any amino acid"

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Location/Qualifiers

Misc-difference

Synthetic

Misc-difference

Misc-difference Misc-difference

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ALIGNMENTS

Binding site motif used in inhibition of receptor cleavage.

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Signal transduction, proteolytic cleavage, binding site motif, ubiquitin, proteosome binding site, muscle wasting, renal tubular defect, uraemia,
rd; peptide; 8 AA
                                                             09-NOV-1999 (first entry)
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Human exp Human exp Arabidops Pk-15-Por Novel pro Photorhab BmNPV ina BmNPV ina Oropouche Staphyloc White clo Staphyloc Staphyloc Protein e Arabidops Arabidops Arabidops лмап 1ут Photorhab Protein e isteria Anemonia Lung Aap90048 1 Aap90122 1 Aap90372 1 Abb48964 1 Abu04228 1 Abu04231 Abm72574 Abm34185 Abm2268 Abm68207 Abm68207 Adc51648 Adc51648 Abm67008 Abm67008 Abm67008 Aag24783 ; Abu02916 ; Aab65699 ; Abb63794 I Abu33571 Abb38713 Abb96274 Aabb6523 Abm69271 Aaw76226 Aaw76226 Adm69364 I Abb50024 I Abb50024 I Abb50024 I Abb50024 I Abb50024 I Abb69364 Aag43175 I Aag12208 Aae25084 Aag46861 Aag11114 Aag09384 Abp46085 Abp98019 Abp98019 Aaw60261 | Aay26170 (Aab58174 ) Aab34702 Aag43174 Aaw30684 Aab74888 Abu26653 Aag10426 Abp30356 Aay34658 Abb60828 AAP90372 ABB48964 AAG24783 ABU02916 AAG11114 AAG09384 AAG51126 ABP46085 AAG12208 AAE25084 AAY26170 AAB58174 AAB34702 AAB74888 AAY34658 ADC00386 AAE28840 AAW99090 **ABM67008** AAG36955 AAB65699 **ABB63794** ABU43457 ABP38713 AAB16523 AAW76226 AAG46861 ABP96274 ADA36041 ABM69364 AAG43175 ABP98019 AAW57328 ABM69271 ABB50024 AAW30684 AAW60261 AAG10426 ABP30356 ABB60828 AAG43174 

Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.

98EP-00200799. 98EP-00200799

12-MAR-1998; 12-MAR-1998;

22-SEP-1999 EP943624-A1

(UYUT-) RIJKSUNIV UTRECHT

WPI; 1999-510568/43.

Claim 10; Page 27; 36pp; English.

Human kin Arabidops Arabidops Photorhab Arabidops Arabidops Arabidops Human BLy canc Chlamydia Enterohae Bacteriop Photorhab Acinetoba Arabidops Mitochond Cytosolic Human sec Saccharom Protein e Bacterial Arabidops Streptoco Amino aci Klebsiell Drosophi] glutami glutami Listeria ycerol

This sequence is a binding site motif. This motif is used in a method for controlling the availability and signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage of the receptor. Inhibition of this proteolytic cleavage results in the receptors being present on the surface for longer and therefore signalling for longer to the interior of the cell. This increases the sensitivity of cells to any hormones which might be present. The binding motif, is located at or around a ubiquitin and/or ubiquitin/proteosome complex binding site. The inhibitor of the method is either derived from, competes with, or binds to this binding motif. The inhibitor may be used to treat muscle wasting, associated with disorders such as renal tubular defects, uraemia, diabetes, Gushing's syndrome, cachexias, eating disorders, AIDS, after stress and during neuromuscular disease

100.0%; Score 25, DB 2; Length 8; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels 8; Conservative Query Match Best Local Similarity Best Loc Matches à

Sequence 8 AA;

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AAY32800 standard; peptide; 12 AA 09-NOV-1999 (first entry) RESULT 2
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KW Sign
KW Giab
KW Grow
XX

Immunoglobulin E (IgE) receptor polypeptide.

Signal transduction; proteolytic cleavage; IgE receptor; proteosome binding site; muscle wasting; renal tubular defect; uraemia; diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin; growth hormone deficiency; inhibitor; immunoglobulin E.

EP943624-A1 22-SEP-1999

Synthetic.

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This sequence is derived from the growth hormone receptor polypeptide
AAY32792. This sequence and variants (AAY32794-Y32823) of it are examples
of polypeptide sequences found at or near the ubiquitin/proteosome
binding site located on the intracellular part of a cell surface
comport. These sequences are used in a method for controlling the
receptor. These sequences are used in a method for controlling the
availability and signal transduction capability of a cell surface
creceptor by administering an inhibitor that is capable of inhibiting
proteclytic cleavage of the receptor. Inhibition of this proteclytic
cleavage results in the receptors being present on the surface for longer and therefore signalling for longer to the interior of the cell. This
increases the sensitivity of cells to any hormones which might be
concreased the inhibitor is either derived from, competes with or binds to
a polypeptide sequence of which sequences AAY32323 are examples.
The inhibitor may be used to treat muscle wasting, associated with
disorders such as renal tubular defects, uraemia, diabetes, Cushing's
syndrome, cachesias, eating disorders, AIDS, after stress and during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Growth hormone receptor; signal transduction; proteolytic cleavage; ubiquitin; proteosome binding site; muscle wasting; renal tubular defect; uraemia; diabetes; Cushing's disease; eating disorder; AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth hormone receptor polypeptide for inhibition of receptor cleavage.
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                                                                         Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 2; Length 12;
Pred. No. 1.8e+02;
Mismatches 0; Indels
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4; Mismatches
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                                                                                                                                                                            Disclosure; Page 5; 36pp; English.
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                         WPI; 1999-510568/43.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is a polypeptide from the immunoglobulin E receptor.

Sequences (AAX32794-Y32823) are examples of polypeptide sequences found

at or near the ubiquitin/proteosome complex binding site located on the

intracellular part of a cell surface receptor. These sequences are used

in a method for controlling the availability and signal transduction

capability of a cell surface receptor by administering an inhibitor that

capable of inhibiting proteolytic cleavage of the receptor. Inhibition

of this proteolytic cleavage results in the receptors being present on

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                                                                                                                                                                                                                                                                                                                                                                                                                               Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 9; 36pp; English.
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5 GEFIWVDG 12
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                                                                                                                                                                                         12-MAR-1998;
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Query Match Matches

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EP943624-A1 22-SEP-1999

Mammalia.

AAY32793;

RESULT

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Gaps .,

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This sequence is a polypeptide from the chicken growth hormone receptor. Sequences (AAY32794-Y32823) are examples of polypeptide sequences found at or near the ubiquitin/proteosome complex binding site located on the intracellular part of a cell surface receptor. These sequences are used in a method for controlling the availability and signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteclytic cleavage of the receptor. Inhibition of this proteclytic cleavage results in the receptors being present on the surface for longer and therefore signalling for longer to the interior of the cell. This increases the sensitivity of cells to any competes which might be present. The inhibitor is either derived from, competes which might be present. The inhibitor may be used to treat muscle AAY37794-Y32823 are examples. The inhibitor may be used to treat muscle wasting, associated with disorders such as renal tubular defects,
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signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage of the receptor. Inhibition of this proteolytic cleavage results in the receptors being present on the surface for longer and therefore signalling for longer to the interior of the cell. This increases the sensitivity of cells to any hormones which might be present. The binding motif, of which this sequence is an example, is located at or around a ubsquitin and/or ubiquitin/proteosome complex binding site. The inhibitor of the method is either derived from, competes with, or binds to this binding motif. The inhibitor may be used to treat muscle wasting, associated with disorders such as renal tubular defects, uraemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS, after stress and during neuromuscular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal transduction; proteolytic cleavage; growth hormone receptor; proteosome binding site; muscle wasting; renal tubular defect; uraemia; diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin; growth hormone deficiency; inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.
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Pred. No. 1.8e+02;
;) Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken growth hormone receptor derived polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY32794 standard; peptide; 12 AA.
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50.0%; rr.
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5 VEFIELDI 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           1 XEFIXXDX
                                                                                                                                                                                                                                                                                               Sequence 12 AA;
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The invention describes a purified polypeptide, which comprises a transporter, cytoskeletal protein, receptor or transcription factor. The transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified colypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I in Mic-binding polypeptide. The polypeptide as and polypeptide are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Translational profiling, expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
uraemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS, after stress and during neuromuscular disease
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                                                                                                                                                                 Length 12;
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                                                                                                                                                          Score 25; DB 2;
Pred. No. 1.8e+02;
4; Mismatches 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human expressed protein tag (EPT) #73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Urban RG;
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                                                                                                                                                                                                                             4;
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2001US-0292544P.
2001US-0310801P.
2001US-0326370P.
2001US-0336780P.
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50.0%;
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                                                                                                                                                                                                                             Conservative
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5 VEFIELDI 12
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                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                             Sequence 12 AA;
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08-AUG-2001;
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04-DEC-2001;
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ABP42844 standard; protein; 36 AA.
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specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assays for identifying regulators of cell cycle progression - comprise expressing a protein having a transcription factor nuclear localisation signal and determining the degree of nuclear localisation.
                                                                                                                                                                                                            Gaps
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                                                                                                                                                Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine DP-3 protein E region nuclear localisation signal.
                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nuclear localisation signal; NLS; mouse; murine.
                                                                                                                                                Score 25; DB 6;
Pred. No. 1.9e+02;
                                                                                                                                                                                                            Mismatches
                                 ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                         4;
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50.0%; F
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                                                                                                                                                                                                            Conservative
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GEFIWVDG 9
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                                                                                                                                                                  Local Similarity
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                                                                                             Sequence 13 AA;
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The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also cencempasses polypeptides 90% identical and polynucleotides 99% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen to polynucleotides, antibodies against human ovarian antigens and the use of ovarian antigens of ovarian antigens, and the use of ovarian polynucleotides and polypeptides in diagnosing, treating, prognosing or perventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and clisorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorthoea), endocrine disorders, infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorthoea, endocrine cshock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired chooseficiencies, autoimmune ophoritis, systemic lupus erythematosus), cshock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and untimnary system disorders. (e.g., anaemia), cardiovascular disorders. December of confounder ovarian antigen expression or activity. The polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may be used as food additives or to prepare antibodies cuseful in disease diagnosis, dry targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence cepresents a human ovarian antigen of the printed in electron, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                              Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                      Human ovarian antigen HPCRN90, SEQ ID NO:3976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 3976; 2922pp; English.
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                                                                                            22-AUG-2002
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Gaps

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4; Conservative

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1 XEFIXXDX 8

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(first entry)

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Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes encoding secreted polypeptides.
                                                                Human secreted protein encoded by gene 96.
AAY36319 standard; protein; 45 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-418749/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAX98011
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                         WO9931117-A1
                                                                                                                                                                                                                                    17-DEC-1998;
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19-DEC-1997;
19-DEC-1997;
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18-DEC-1997;
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                                           17-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrie AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Moore PA,
                     AAY36319
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kyaw H,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX30724 to AAX30946 represent genomic DNA sequences isolated from Streptococcus pneumoniae strain 0100993. These genomic DNA sequences encode the novel proteins given in AAY1114 to AAY11367. The proteins, isolated from Streptococcus pneumoniae, can be used in vaccines against streptococcal infections and in assays for identifying compounds that inhibit or activate the activity of the proteins. The antagonists can be used to treat an individual having need to inhibit a bacterial protein. Vectors expressing the proteins can be used to induce a protective immune response in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding pneumococcal polypeptide(s) - useful in vaccines,
                                                                  Gaps
                                                                                                                                                                                                                                                        pneumoniae strain 0100993; vaccine; immune response; infection; pneumococcal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 2; Length 37; 50.0%; Pred. No. 5.7e+02; ive 4; Mismatches 0; Indels
                                            Length 36;
                                         Score 25; DB 5; Length 36
Pred. No. 5.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                     Streptococcus pneumoniae protein sequence ID NO:363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Knowles DJC, Nicholas RO,
at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                    AAY11253 standard; protein; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 279; 354pp; English.
                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                           100.0%; I
                                                                                                                                                                                                                                                                                                                                                                                             96US-0025788P.
                                                                                                                                                                                                                                                                                                                                                              97WO-US005306
                                                                                                                                                                                                                                                                                                                                                                                   96US-0014690P.
                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae.
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hodgson JE,
                                                                                                   :|||::|:
QEFIDDDK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-503111/46.
                                                                                      1 XEFIXXDX 8
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Best Local Similarity
                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37 AA;
                      Sequence 36 AA;
                                                                                                                                                                                                                                                                       streptococcal
                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-1996;
                                                                                                                                                                                                                                                                                                                  WO9737026-A1
                                                                                                                                                                                                                                                                                                                                                              01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                  02-APR-1996;
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                                                                                                                                                                                         AAY11253;
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                                                                 Matches
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97US-0068006P. 97US-0068003P. 97US-006803B. 97US-0068054P. 97US-0068054P. 97US-0068064P. 97US-0068169P. 97US-0068169P.

97US-0068368P 97US-0068369P

98WO-US027059

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AXY97916 to AAXY98029 represent 110 isolated human secreted protein genes.
AXY36224 to AAXJ8727 represent the secreted proteins encoded by the 110 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliotating secreted polypeptides are by protein or gene therapy. Also pathological conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 110 genes, based on which tissues they are most highly expressed in, and include developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alabeimer, sand cognitive disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, atherosclerosis, disorders, infections and AlDS. The polypeptides are also useful for identifying their binding partners. The sequences given the AXX97907 to AAX97915 and AAX16223 are used in the exemplification of
Claim 11; Page 401; 537pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention
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DB 2; Length 45;

100.0%; Score 25; DB 2; 50.0%; Pred. No. 7e+02;

Query Match Best Local Similarity

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Gaps

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4; Conservative

Matches

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RESULT 10 AAY36319

1 XEFIXXDX 8

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Feng P;

Soppet DR; Greene JM,

, Rosen CA, Florence C,

Shi Y,

Ruben SM, Carter KC, carei Y, Florence K, Duan RD, Tanat F, Ni J;

Wei Y,

. 0

Gaps

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Indels

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7e+02;

Matches

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The present sequence is that of amino acids 7-54 of a phospholipid transporter consensus sequence, denoted ATPase hydrolase phosphorylation transporter consensus sequence, denoted ATPase hydrolase phosphorylation. This sequence shows 564 identity with a phospholipid-transporting multigene. This sequence shows 564 identity with a phospholipid-transporter of the invention, designated 67108 (see ABP72495). The invention provides 67108 nucleic acids and polypeptides, vectors, host cells, antibodies and transgenic animals. The 61708 nucleic acids and polypeptides are useful for diagnosing, preventing or treating conditions related to aberrant activity or deficient phospholipid transporter function or expression, such as neurological disorders, callular proliferative and/or differentiative disorders, immune disorders, inflammatory disorders, viral diseases, cardiovascular disorders, blood coagulation disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New 61708 nucleic acid molecules and polypeptides, useful for diagnosing or treating conditions related to aberrant activity or deficient phospholipid transporter function or expression, e.g. autoimmune disease,
  increase or decrease storage capabilities, fat content or other nutritional components. The present sequence represents the amino acid sequence of a novel human secreted protein. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov.uk/sequence.html?DocID=20030055236.
                                                                                                                                                                                                             Score 25; DB 6; Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phospholipid transporter; ATPase; enzyme; 67108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phospholipid transporter consensus sequence.
                                                                                                                                                                                                                                Pred. No. 7e+0
4; Mismatches
decrease storage capabilities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 66; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP72498 standard; protein; 48 AA.
                                                                                                                                                                                                           100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                  50.0%;
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Matches 4; Conserv
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                                                                                                                                                                  AA;
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                                                                                                                                                                  Sequence 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated HXABT24 nucleic acid molecule. The polypeptides, mucleic acids and antibodies are useful for diagnosing a pathological condition.

For preventing, treating, or a meelicrating a medical condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probbs for differential identification of the tissues immunological probbs for differential identification of the tissues immunological probbs for differential identification dispense assays. The polypeptide, polynucleotide, agonist or antagonist may also be used as a food additive or preservative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New secreted HKABT24 nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soppet DR;
Greene JM,
  0;
                                                                                                                                                                                                                                                                                                                                                                                  cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive; food preservative; storage capability; fat content; nutritional component; human; secreted protein.
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carter KC, Shi Y, Rosen CA,
ence KA, Duan DR, Florence C,
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                                                                                                                                                                                                                                                                                                                                          Human novel secreted protein, SEQ ID NO 208.
  Mismatches
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                                                                                                                                                                                                    ADA11680 standard; protein; 45 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Florence KA, Duas
Janat F, Ni J;
  4,
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97US-0068008P.
97US-0068053P.
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97US-0068064P.
97US-0070923P.
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97US-0068365P.
97US-0068367P.
97US-0068368P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US027059
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4; Conservative
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                                          1 XEFIXXDX
                                                                                     25 IEFIAADF
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Ferrie AM, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADA11556.
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18-DEC-1997, 18-DEC-1997,

18-DEC-1997; 18-DEC-1997 19-DEC-1997 19-DEC-1997 19-DEC-1997 19-DEC-1997 19-DEC-1997 17-JUN-1999

Moore PA,

disorders

sapiens.

Homo

20-MAR-2003

18-DEC-1997 18-DEC-1997 18-DEC-1997

06-NOV-2003

ADA11680;

RESULT 11 ADA11680 .;

Gaps

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Length 48;

100.0%; Score 25; DB 6; Length 48 50.0%; Pred. No. 7.5e+02; ive 4; Mismatches 0; Indels

4; Conservative

Query Match Best Local Similarity Matches 4; Conserv

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The present invention relates to a new protein with scaffold structure of c-type lectin-like domains (CTLD). The invention comprises a variant of a model CTLD where alpha-helices and beta-strands and connecting segments are conserved such that scaffold structure of C-type lectin-like domains are conserved such that scaffold structure of C-type lectin-like domains (CTLD) is substantially maintained, while the 14loop region is altered by amino acid substitution, deletion, insertion or their combination. The invention is useful for preparing a library of nucleotide sequences conding related proteins by randomising part or all of the nucleic acid protein products are preferable to antibody derivatives as each binding components of compositions to be used for in vivo diagnostic or therapeutic purposes, arrificial CTLD protein domain. When used as components of compositions to be used for in vivo diagnostic or therapeutic purposes, arrificial CTLD protein products constructed on the cases of human CTLDs are virtually identical to the corresponding natural communogenic to the patient. They also have a smaller size, and thus provide tissue penetration and distribution, as well as shorter half life in circulation. Since murine and human tetranectin are identical in the invanion of plyapeptide segments defining certify any of any passenticity between murine and human tetranectin corresponding the present amino acid sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein comprising a variant of model C-type lectin-like domains (CTLD), in which alpha helices, beta-strands, connecting segments are conserved to maintain CTLD scaffold structure, while the loop region is altered.
                                                                                                                                                                                                                                                                                                Scaffold protein; C-type lectin-like domain; CTLD; alpha-helix; beta-strand; connecting segment; 14loop region; tetranectin; ligand-binding specificity; human; mouse; rat; chicken; trout; cow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thogersen HC;
                                                                                                                                                                                                                                                          C-type lectin-like domain protein IGE-FCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graversen NJH,
                                                                                                                                   ABG80735 standard; protein; 54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 5; 168pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-2000; 2000DK-00001872.
28-FEB-2001; 2001US-0272098P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-2001; 2001WO-DK000825
                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BORE-) BOREAN PHARMA AS
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                         : | | | :: | :
DEFIPADL 26
  1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                                                                                                                                       WO200248189-A2.
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                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                     29-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Etzerodt M,
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The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Heia cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                    Peptide #3126 encoded by probe for measuring cervical gene expression.
                                                                                                                                human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 8.8e+02;
; Mismatches 0; Indels
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                        AAM16692 standard; protein; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB35677 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                                                                                                                                     2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US000670.
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2000US-00608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
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37 QEFINLDG 44
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Best Local Similarity
                                                                                                                                              cervical cancer.
                                                                                                                                                                                                 WO200157278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 56 AA;
                                                                                                                                                                        Homo sapiens.
                                                                             12-OCT-2001
                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                            26-MAY-2000;
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27-SEP-2000;
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                                                   AAM16692;
                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB35677;
                                                                                                                                   Probe;
RESULT 14
AAM16692
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4; Conservative

Matches

Query Match Best Local Similarity

0

Gaps

0;

100.0%; Score 25; DB 5; Length 54; 50.0%; Pred. No. 8.5e+02; ive 4; Mismatches 0; Indels

09-AUG-2001

Penn SG,

Human gene

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New spatially-addressable set of single exon nucleic acid probes, useful
                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #3165 encoded by breast cell single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 4; L
50.0%; Pred. No. 8.8e+02;
cive 4; Mismatches 0;
                                                                                                                                                                                                                                                                                Claim 27; SEQ ID NO 29448; 654pp; English.
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                                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB30514 standard; peptide; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
               26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053266.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0180312P.
2000US-0207456P.
2000US-00608408.
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2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                  Chen W,
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2000US-0180312P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                human genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||::|:
QEFINLDG 44
                                                                                                                                                                   Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 XEFIXXDX 8
                                                                                                                                                                                                  WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 17
ABB30514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a poptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #3216 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                   Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·.
                      Peptide #3183 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 28312; 639pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                      Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression in human fetal liver
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50.0%; F
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2000US-00608408.

2000US-00632366.

2000US-0234687P.

2000US-0236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 QEFINLDG 44
                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 XEFIXXDX 8
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157272-A2
                                                                                                                            WO200157277-A2.
                                                                                                                                                                                                                                                                         03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                           30-JUN-2000;
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                                                                                                                                                                                                                          04-FEB-2000;
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                                                                                           Homo sapiens
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AAM29179;

RESULT 16 AAM29179

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0

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
   for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                    SEQ ID NO 13482; 327pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 56 AA;
                                                                                    Claim 27;
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0 ; Score 25; DB 4; Length 56; Pred. No. 8.8e+02; 4; Mismatches 0; Indels 100.08; 50.0%; 4; Conservative :|||::|: QEFINLDG 44 1 XEFIXXDX 8 Local Similarity Query Match Matches 염

ABB21106 standard; protein; 56 AA. (first entry) 23-JAN-2002 ABB21106; RESULT 18 ABB21106 

Protein #3105 encoded by probe for measuring heart cell gene expression. Human, gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.

Homo sapiens

WO200157274-A2

30-JAN-2001; 2001WO-US000666 09-AUG-2001

26-MAY-2000, 2000US-0207456F. 30-UUN-2000, 2000US-00608408 03-AUG-2000, 2000US-00632866. 21-SEP-2000, 2000US-0234687P. 27-SEP-2000, 2000US-02368359P. 2000US-0180312P 04-FEB-2000;

(MOLE-) MOLECULAR DYNAMICS INC.

2000GB-00024263,

04-OCT-2000;

2000US-0236359P

Rank Chen W, Hanzel DK, Penn SG,

DR;

WPI; 2001-488899/53

Single exon nucleic acid probes for analyzing gene expression in human hearts.

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, taging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular diseases of the hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
                        Claim 15; SEQ ID NO 22876; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Gaps . 100.0%; Score 25; DB 4; Length 56; 50.0%; Pred. No. 8.8e+02; ive 4; Mismatches 0; Indels Conservative 37 QEFINEDG 44 æ Local Similarity 1 XEFIXXDX Query Match Matches ð

.; 0

RESULT 19

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Gaps

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AAM68870 standard; protein; 56 AA. AAM68870

(first entry) 06-NOV-2001 AAM68870;

Human bone marrow expressed probe encoded protein SEQ ID NO: 29176.

Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.

Homo

WO200157276-A2.

09-AUG-2001

30-JAN-2001; 2001WO-US000668.

2000US-0207456P. 2000US-00608408. 2000US-00632366. 2000US-0234687P 2000GB-00024263 04-FEB-2000; 26-MAY-2000; 30-JUN-2000; 21-SEP-2000; 27-SEP-2000; 04-OCT-2000; 

(MOLE-) MOLECULAR DYNAMICS INC

Chen W, Rank DR; Hanzel DK, Penn SG,

WPI; 2001-488900/53.

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow

Example 4; SEQ ID NO 29176; 658pp + Sequence Listing; English.

probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention The present invention provides a number of single exon nucleic acid

AAM56491;

AAM56491 RESULT

g δ

Matches

X 8

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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. C(1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG9930 represent human colliformation for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #3091 encoded by probe for measuring breast gene expression.
                                                                                                                                Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 4; Leur
No. 8.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 29179; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                  Human liver peptide, SEQ ID No 29179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank
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ABGS0531 standard; peptide; 56 AA.
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; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-023687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US000664
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                                                                   (first entry)
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37 QEFINLDG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 XEFIXXDX 8
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                            WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                           26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                   25-FEB-2003
                                                                                                                                                                                                                                                          09-AUG-2001
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                                     ABG50531;
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BXEXXXX
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                                                                                         0
                                                                                                                                                                                                                                                                                                                                                Human brain expressed single exon probe encoded protein SEQ ID NO: 28596.
                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Score 25; DB 4; Length 56; Pred. No. 8.8e+02; 4; Mismatches 0; Indels
                                                       Score 25, DB 4; Length 56;
Pred. No. 8.8e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank
                                                                                                                                                                                                                                                   AAM56491 standard; protein; 56 AA.
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26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608498.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000GB-00024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.08;
                                                                              50.0%;
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                              Conservative
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QEFINLDG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 XEFIXXDX 8
                                                                                                                                                                 37 QEFINLDG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-483446/52
                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                              Query Match
Best Local Similarity
                                                                                                                               1 XEFIXXDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                       05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                            Sequence 56
                                                                                                  4;
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Penn SG,

(MOLE-)

. 0

Gaps

· 0

37

Matches

à Dp RESULT 21 ABG50531

Length 56; Indels primary ciliary dyskinesis; pulmonary hypertension;

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The present invention relates to novel single exon nucleic acid probes (see AA100010-AA10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a predicting, diagnosing, stading, stading, monitoring and prognesing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include breast cancer, disorders of development inflammatory diseases include breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                   Novel single exon nucleic acid probe used to measuring gene expression in
                              inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                 breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; SEQ ID NO 13149; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
                                                                                                                                                                                   ; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                             21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
                                                                                                                                                      29-JAN-2001; 2001WO-US000661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 56 AA;
                                                                                           WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     a human breast
                                                              Homo sapiens
                                                                                                                                                                                                     26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                              03-AUG-2000;
                                                                                                                                                                                     04-FEB-2000;
                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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ö Human peptide encoded by genome-derived single exon probe SEQ ID 28116. chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; Gaps Human; single exon probe, asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; ; 0 ; Score 25; DB 4; Length 56; Pred. No. 8.8e+02; 4; Mismatches 0; Indels ABG38451 standard; peptide; 56 AA. (first entry) 37 QEFINLDG 44 1 XEFIXXDX 8 19-AUG-2002 ABG38451; RESULT 23
ABG38451
ID ABG384
XX
AC ABG38
AC ABG38
DT 19-AU
XX
XX
DE Human
XX
KW Human
XX
KW chrin
KW chrin
KW tuber
KW tuber
KW Herman
KW Herman
KW Herman

Length 56;

100.0%; Score 25; DB 5; 50.0%; Pred. No. 8.8e+02;

Query Match Best Local Similarity

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The invention features to a spatially-addressable set or single exon mucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung; measuring are expression in a sample collection of detectably labeled nucleic acids derived from human lung contracting the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a eukaryotic genome, comprising (a) array; identifying at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridiation of detectably labeled nucleic acids from eukaryote; bung meanury a single exon probe in the above mentioned microarray; assigning exons to a single exon probe having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the expression of the exons in the tissues and/or cell types using hybridisation to a single gene; a peptide comprising one collectived mentaling frames (ORP). The probes are used for identifying exons in a gene, particularly using human cancer, chronic obstructive pulmonary diseases (DOPD), interstrial lung derived mentaling indopathic pulmonary envised mentaling is unlamental mulmonary mulmonary envisementalin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is a peptide/protein encoded by a single exon probe of
the invention. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Puddak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histicocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spatially-addressable set of single exon nucleic acid probes, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 28116; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank DR;
                                                                                                                                                                                                                                                                                     26-MAY-2000; 2000US-0207455F.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02345897P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                      2000US-0180312P
                         hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-114183/15.
                                                                                                                    WO200186003-A2.
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                                                                         Homo sapiens.
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                                                                                                                                                                    15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
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Matches

à 셤 RESULT 24

AAG02282

Human;

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                  Arabidopsis thaliana protein fragment SEQ ID NO: 8815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9905-0135529-
9905-0135529-
9905-01367219-
9905-01367829-
9905-0137228-
9905-0137228-
9905-01377528-
9905-01377528-
9905-01377544-
9905-01385409-
9905-01385409-
9905-01385409-
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9905-0132407P
9905-0132484P
9905-0132486P
9905-0132486P
9905-0132487P
9905-0134218P
9905-0134218P
9905-0134218P
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99US-0134941P.
99US-0135124P.
                                                                                                                                                                                                                                                                                                   990S-0126785P.
990S-0127462P.
99US-0128234P.
99US-0128714P.
99US-0129845P.
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99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
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99US-0139455P.
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99US-0139460P
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99US-0131449P.
                                                                                                                                                                                                                                                                                                                                                                                     99US-0130449P
                                                                                                                                                                                                         2000EP-00301439
           17-OCT-2000 (first entry)
                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-1999;
                                                                                                                                                                                                         25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,666
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08-JUN-1999;
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                                                                                                                                                    EP1033405-A2
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                                                                                                                                                                               06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JUN-1
The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited from isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can threfore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
 ó
                                                                                                                                                                                                                                      expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 100.0%; Score 25; DB 3; Length 57; Similarity 50.0%; Pred. No. 8.9e+02; 4; Conservative 4; Mismatches 0; Indels
  Indels
 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duclert A, Giordano J;
  Mismatches
                                                                                                                                                                                                            Human secreted protein, SEQ ID NO: 6363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG10476 standard; protein; 57 AA.
                                                                                                                           AAG02282 standard; protein; 57 AA
                                                                                                                                                                                                                                                        gene therapy; chromosome mapping.
    4.
                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2000; 2000EP-00200610.
                                                                                                                                                                                                                                                                                                                                                                                               99US-0122487P.
                                                                                                                                                                                    (first entry)
 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEFILIDE 46
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37 QEFINLDG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 XEFIXXDX 8
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                             1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAC02288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 57 AA;
                                                                                                                                                                                                                                        5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-1999;
                                                                                                                                                                                                                                                                                                             EP1033401-A2.
                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                     06-OCT-2000
                                                                                                                                                                                                                                                                                                                                        06-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches

RESULT 25

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AAG10476

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990S-0139750P.
990S-0139763P.
990S-0139899P.
990S-0140353P.
990S-0140853P.
990S-0141287P.
990S-0141287P.
990S-0142280P.
990S-0142280P.
990S-014232P.
990S-014232P.
990S-014232P.
990S-0144332P.
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13-AUG-1999;
17-AUG-1999;
18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
25-AUG-1999;
18-70N-1999;
18-70N-1999;
22-70N-1999;
23-70N-1999;
23-70N-1999;
24-70N-1999;
28-70N-1999;
30-70N-1999;
01-70L-1999;
01-70L-1999;
01-70L-1999;
02-70N-1999;
                                                                                                              09-JUL-1999;
12-JUL-1999;
13-JUL-1999;
14-JUL-1999;
15-JUL-1999;
16-JUL-1999;
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19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
20-JUL-1999;
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21 - 70L - 1999;
22 - 70L - 1999;
22 - 70L - 1999;
22 - 70L - 1999;
23 - 70L - 1999;
23 - 70L - 1999;
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26-JUL-1999;
27-JUL-1999;
27-JUL-1999;
27-JUL-1999;
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-AUG-1999;
-AUG-1999;
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02-AUG-1999;
03-AUG-1999;
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04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
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                                                                                                         JUL-1999
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 28238.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25; DB 3; L
Pred. No. 8.9e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG24529 standard; protein; 57 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
9908-0151065P.
9908-01510806P.
9908-0151303P.
9908-0151333P.
9908-0151330P.
9908-015370P.
9908-0154039P.
9908-0154039P.
9908-0154039P.
9908-0154039P.
9908-0155486P.
9908-0155486P.
9908-0155486P.
9908-0155486P.
9908-0155486P.
9908-015522P.
9908-015923P.
9908-015923P.
9908-0159284P.
9908-0159284P.
9908-0159284P.
9908-0159284P.
9908-0160341P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
larity 50.0%;
Conservative 4
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IEFICLDL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 XEFIXXDX
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
31-AUG-1999;
01-SEP-1999;
110-SEP-1999;
13-SEP-1999;
                                                                                                                 24. SEP-1999

28. SEP-1999

29. SEP-1999

04. OCT-1999

06. OCT-1999

07. OCT-1999

13. OCT-1999

13. OCT-1999

14. OCT-1999

14. OCT-1999

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                                                                          -SEP-1999;
-SEP-1999;
-SEP-1999;
-SEP-1999;
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Matches
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28-JUN-1999; 29-JUN-1999; 30-JUN-1999; 01-JUL-1999; 02-JUL-1999; 06-JUL-1999; 08-JUL-1999; 08-JUL-1999;	PR 14-UL-1999; 99US-0144085P. PR 14-UL-1999; 99US-0144086P. PR 16-UL-1999; 99US-0144086P. PR 19-UL-1999; 99US-0144086P. PR 19-UL-1999; 99US-0144086P. PR 19-UL-1999; 99US-0144332P. PR 19-UL-1999; 99US-0144332P. PR 20-UL-1999; 99US-0144332P. PR 20-UL-1999; 99US-0144332P. PR 20-UL-1999; 99US-0144332P. PR 21-UL-1999; 99US-0144332P. PR 22-UL-1999; 99US-0144332P. PR 22-UL-1999; 99US-0144884P. PR 22-UL-1999; 99US-0144884P. PR 22-UL-1999; 99US-0144884P. PR 22-UL-1999; 99US-0145085P. PR 22-UL-1999; 99US-0145088P. PR 22-UL-1999; 99US-0145088P. PR 22-UL-1999; 99US-0145088P. PR 22-UL-1999; 99US-014518P. PR 23-UL-1999; 99US-014518P. PR 02-AUG-1999; 99US-014518P. PR 02-AUG-1999; 99US-014518P. PR 02-AUG-1999; 99US-014518P. PR 02-AUG-1999; 99US-014531P. PR 13-AUG-1999; 99US-01448341P. PR 12-AUG-1999; 99US-014884P. PR 13-AUG-1999; 99US-014884P. PR 12-AUG-1999; 99US-0149834P. PR 12-AUG-1999; 99US-014984P. PR 12-AUG-1999; 99US-014984P. PR 12-AUG-1999; 99US-014984P. PR 12-AUG-1999; 99US-01498	01-SEP-1999; 07-SEP-1999;
nce. ana. EP-00301439.	990S-0121825P. 990S-0123180P. 990S-0123180P. 990S-0125788P. 990S-0126264P. 990S-0126264P. 990S-0128234P. 990S-0128234P. 990S-0128234P. 990S-0130077P. 990S-0132407P. 990S-013421P. 990S-0134221P. 990S-0134224P. 990S-0134224P. 990S-0134234P. 990S-0139455P.	JS-0140354P. JS-0140695P.
termination sequence Arabidopsis thaliana EP1033405-A2. 06-SEP-2000. 25-FEB-2000; 2000EP-	PR 25-FZB-1999	166

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The present invention describes an Oropouche NP (nucleocapsid) protein. The Oropouche virus belongs to the genus Bunyavirus of family Bunyaviridae. The Oropouche NP protein can be used to detect anti-NP antibodies, for diagnosis of Oropouche virus infection and for protein is used to design: (i) oligonucleotide primers for diagnostic reverse transcription polymerase chain reaction (RT PCR) of viral RNA in infected cell cultures or serum samples; or (ii) probes for hybridisation reactions with viral RNA. Also, the nucleic acid sequence may be used in vaccines to protect against Oropouche virus infection. The present sangles and Oropouche virus infection. The present plasmid, which is used in an example from the present invention. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                              New DNA encoding the nucleocapsid protein of Oropouche virus - used for diagnosing Oropouche virus infection and in vaccines against this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #10727 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 25; DB 2; Length 58; Pred. No. 9.1e+02; 4; Mismatches 0; Indels
                                                                                                            Wang H;
                                                                                                            Shope RE,
                                                                                                            Tesh RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB43221 standard; peptide; 60 AA.
                                                                                                                                                                                                                                        Example 7; Fig 7; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0201456P.
30-UJN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-0033366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
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50.0%; I
                          98WO-US014887.
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                                                      97US-0052848P.
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                                                                               (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                            Barrett ADT, Saeed MF,
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41 SEFIFNDV 48
                                                                                                                                      WPI; 1999-132152/11.
N-PSDB; AAX19099.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 58 AA;
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                                                      17-JUL-1997;
                         17-JUL-1998;
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28-JAN-1999
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99US-0160741P.
99US-0160768P.
99US-0160768P.
99US-0160814P.
99US-0160814P.
              99US-0153758P.
99US-0154018P.
99US-0154039P.
99US-0155139P.
99US-015568P.
99US-0155659P.
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99US-0159330P.
99US-0159331P.
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99US-0157753P.
99US-0157865P.
99US-0158029P.
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99US-0159294P.
99US-0159295P.
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99US-0158369P.
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04-JUN-1999 (first entry)
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Best Local Similarity 50.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|||::|:
31 IEFICLDL 38
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Unidentified.
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                                                                                                                                                                  06-0CT-1999;
07-0CT-1999;
08-0CT-1999;
12-0CT-1999;
13-0CT-1999;
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14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
21-0CT-1999;
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21-OCT-1999;
21-OCT-1999;
              13.SEP-1999;
15.SEP-1999;
20.SEP-1999;
22.SEP-1999;
23.SEP-1999;
24.SEP-1999;
26.SEP-1999;
26.SEP-1999;
26.CEP-1999;
05.OCT-1999;
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21-OCT-1999
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22-OCT-1999
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25-OCT-1999
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25-OCT-1999
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26-0CT-1999
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predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                    Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                             : | | | :: | :
37 TEFINMDG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                  8
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37 TEFINMDG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488900/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 4; Conserv
                                                                                                                  1 XEFIXXDX
                                                Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                              WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
                                                                                                                                                                                                                                          06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                   AAM76953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                         The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for
                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #11098 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                               .;
                                                                                     Claim 27; SEQ ID NO 35856; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                    100.0%; Score 25; DB 4; Length 60; 50.0%; Pred. No. 9.4e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       microarray; human; placenta; antenatal diagnosis;
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              DR;
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              Rank
                                                                                                                                                                                                                                                                                                                                                              AAM37061 standard; protein; 60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression in human placenta.
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            Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                             Conservative
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TEFINMDG 44
            DΚ,
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                                WPI; 2001-483447/52
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                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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            Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic disorder
                                                                                                                                                                                                               Sequence 60 AA;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe;
                                                       Human
            Penn
                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow expressed probe encoded protein SEQ ID NO: 37259.
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        Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 4; Length 60; 50.0%; Pred. No. 9.4e+02; ive 4; Mismatches 0; Indels
                                                        Indels
; Score 25; DB 4; Lo
Pred. No. 9.4e+02;
4; Mismatches 0;
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  100.0%;
50.0%; F
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2000US-00608408.
2000US-00632366.
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 36233.
                                                                                                                                                                                                                                                                                                                 Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 4; Length 60; 50.0%; Pred. No. 9.4e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID No 37263.
                                                           AAM64128 standard; protein; 60 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060B408
33-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0236359P.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
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                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||::||:
37 TEFINMDG 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                          05-NOV-2001
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                                                                                                                          AAM64128;
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RESULT 31
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ABG58615
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                                                               NAMES OF COLOR OF STREET O
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Gaps

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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at fire vipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human peptide encoded by genome-derived single exon probe SEQ ID 35725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interestital lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 25; DB 4; Length 60
Pred. No. 9.4e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID NO 37263; 658pp; English
                                                                                                                                                                                                                                                                                          Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG46060 standard; peptide; 60 AA.
                                                                                                                                                                                                                                                        MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                  30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                  30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                        2000GB-00024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyaline membrane disease
                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 TEFINMDG 44
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Best Local Similarity
Matches 4; Conserv
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              WO200157273-A2
                                                                                                                                                                                                                        04-OCT-2000;
                                                                                                                                    26-MAY-2000;
                                                                                                                    04-FEB-2000;
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                                                09-AUG-2001
                                                                                                                                                                                                                                                                                        Penn SG,
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sapiens

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37 TEFINMDG 44

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(MOLE-) MOLECULAR DYNAMICS INC
                                      03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                               2000US-0207456P.
2000US-00608408.
                   30-JAN-2001; 2001WO-US000665
                                                                  Hanzel DK,
                                                                           WPI; 2002-114183/15.
                                                                                                                                                                                                                                                               Sequence 60 AA;
    WO200186003-A2.
                                   30-JUN-2000;
                                26-MAY-2000;
           15-NOV-2001
                                                                   Penn SG,
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Chen W, Rank DR;

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The invention relates to a spatially-addressable set of single exon muchaic acid probes for measuring gene expression in a sample derived from thuman lung comprising single exon nucleic acid probes having one of romplements our their specification, or their complements our the 12819 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes complements our the 12819 open reading frames derived from the 12614 probes. Also included are a microarray comprising the array with a sample derived from human lung, comprising (a) contacting the array with a sample collection of detectably labeled nucleic acids derived from human lung array. Them is a sample derived from human lung comprising (a) detectably bound to each probe of the array identifying exons in a everatoric genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the ewarayce; and (b) detecting specific hybridisation of detectably labeled nucleic acids from expression of a single exon in the above mentioned microarray; assigning exons to a single exon in the above mentioned microarray; assigning exons to a single exon in the above mentioned microarray; assigning exons to a single exon microarray and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarray having a probe with the exon, where a common pattern of expression of the exons should be assigned to a single gene, a peptide comprising one of the exons should be assigned to a single gene, a periodacity using human lung derived mRNA and for the study of lung diseases such as asthma, lung canner, chronic obstructive pulmonary disease (IDD), intersity using human lung derived mRNA and for the study of lung diseases such as astimated of sucher's disease, Hermansky-histiocytosis, lymphangioleionymonicals, pulmonary dysplasis, prime are periodesis, pulmonary dysplasis, pulmonary dysplasis, pulmonary hypertension and hyaline membrane dise
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25-FEB-2000;
                                                                                                                                                                                                                                                                                           19-APR-1999;
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04-MAY-1999;
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Spatially-addressable set of single exon nucleic.acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 5; Length 60; 50.0%; Pred. No. 9.4e+02; tive 4; Mismatches 0; Indels
                     measure gene expression in human lung samples.
                                                              Claim 27; SEQ ID NO 35725; 634pp; English.
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99US-0139455P

18-JUN-1999

Query Match Best Local Similarity Matches 4; Conservat

1 XEFIXXDX 8

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 42037.
       AAG34535 standard; protein; 61 AA.
                                                                                                                                                                                                   9905-012874P
9905-012874P
9905-0129845P
9905-0130449P
9905-0130449P
9905-0130489P
9905-0131449P
9905-0132484P
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99US-0132486P
99US-0132863P
99US-0132863P
99US-0134218P
99US-0134218P
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9905 0135134P
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99US-0126785P.
99US-0127462P.
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99US-0134370P.
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99US-0138094P.
99US-0138540P.
99US-0138847P.
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99US-0123548P.
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                                   (first entry)
                                                                                           Arabidopsis thaliana
                                                                                                          EP1033405-A2.
                                    18-OCT-2000
                                                                                                                       06-SEP-2000
                     AAG34535;
AAG34535
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9US-0139450P 9US-0139457P 9US-0139459P 9US-0139450P 9US-0139461P 9US-0139461P 9US-0139461P 9US-0139462P 9US-013961P 9US-013963P 9US-0139817P 9US-0139817P 9US-0140154P 9US-0140154P 9US-0140154P 9US-0140154P	990S-0141287P. 990S-0141287P. 990S-0142055P. 990S-0142390P. 990S-0142390P. 990S-0142803P. 990S-0143542P. 990S-0143542P. 990S-0143542P. 990S-0144352P. 990S-0144332P. 990S-0144332P. 990S-0144331P. 990S-0144332P. 990S-0144332P. 990S-0144332P. 990S-0144332P. 990S-0144332P. 990S-0144332P.	9US-0144814P 9US-0145086P 9US-0145086P 9US-0145080F 9US-0145087P 9US-0145087P 9US-0145087P 9US-0145218P 9US-0145218P 9US-0145214P 9US-0145218P 9US-0145918P 9US-0145918P 9US-0145918P 9US-0145918P 9US-0145918P 9US-0145918P	905-014/038P 907-014/204P 908-014/204P 908-014/202P 908-014/416P 908-014/935P 908-0148319P 908-0148319P 908-0148319P 908-0148319P 908-0148319P 908-0148319P
8 - JUN - 1999 8 - JUN - 1999	30-008-1999; 01-008-1999; 02-008-1999; 08-001-1999; 09-001-1999; 12-001-1999; 13-001-1999; 15-001-1999; 16-001-1999; 19-001-1999; 19-001-1999; 19-001-1999; 19-001-1999; 19-001-1999; 20-001-1999; 20-001-1999;	11-001-199 11-001-199 11-001-199 22-001-199 22-001-199 33-001-199 4-001-199 4-001-199 2-001-199 2-001-199 2-001-199 2-001-199	2 - AUG-199 4 - AUG-199 4 - AUG-199 5 - AUG-199 6 - AUG-199 9 - AUG-199 9 - AUG-199 1 - AUG-199 3 - AUG-199 3 - AUG-199 6 - AUG-199 6 - AUG-199
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PR 18-AUG-1999 9918 0419722P.
PR 20-AUG-1999 9918 0419722P.
PR 20-AUG-1999 9918 0419722P.
PR 20-AUG-1999 9918 0419722P.
PR 21-AUG-1999 9918 0419902P.
PR 21-AUG-1999 9918 0419902P.
PR 21-AUG-1999 9918 0419902P.
PR 21-AUG-1999 9918 0419902P.
PR 10-SEP-1999 9918 0419902P.
PR 10-

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Gaps

ABG00521:

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                Arabidopsis thaliana protein fragment SEQ ID NO: 28237.
                                                                                                                                                                                                                                                                                                                                                         9905-0127462P
9905-0128234P
9905-0128714P-
9905-0130077P
9905-0130049P-
9905-0130891P
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9905-0132448P-
9905-0132448P-
9905-0132484P-
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990S 0134256P
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9905-0137222P.
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990S-0139453P.
990S-0139492P.
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99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
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99US-0135629P.
99US-0136021P.
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                                                                                                                                                                                                                              2000EP-00301439
17-OCT-2000 (first entry)
                                                                                                  termination sequence
                                                                                                                                 Arabidopsis thaliana
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 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recarion (PGN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to appear in the printed specification, but was obtained in electronic format directly from WIPO at the sequences

C patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in
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                                                                                                Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 30880; 103pp; English.
                                                                Novel human diagnostic protein #512.
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                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US008631.
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23-AUG-2000; 2000US-00649167.
                                  13-FEB-2002 (first entry)
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Drmanac RT, Liu C,

(HYSE-) HYSEQ INC.

WO200175067-A2. Homo sapiens.

11-OCT-2001.

2001-639362/73

N-PSDB; AAS64708

biodiversity.

:|||::|: 44 QEFINLDG 51

AAG24528;

RESULT 36 AAG24528

1 XEFIXXDX 8

Local Similarity es 4; Conserv

Query Match Best Loc Matches

Sequence 64 AA;

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99US-0139763P
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99US-0140383P
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99US-0140635P
99US-0140635P
99US-0141287P
99US-0141287P
99US-0141287P
99US-014205P
99US-014205P
99US-014205P
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99US-0144036P

99US-0144331P

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99US-0144632P

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99US-0143542P.
99US-0143624P.
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99US-0149723P.
99US-0149929P.
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99US-0150566P.
99US-0150884P.
99US-0151065P.
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18-7UN-1999;
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29-7UL-1999;
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06-AUG-1999;
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12-AUG-1999;
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16-AUG-1999;
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26-AUG-1999;
27-AUG-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 8814.
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9905-0151080P

9905-0151030P

9905-0151303P

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9905-0153070P

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9905-0154039P

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9905-0155486P

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9905-016135P
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50.0%; P
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Matches 4; Conserv
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9905-0140991P.
9905-0141287P.
9905-0142164P.
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9905-0149323P.
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99US-0152363P.
99US-0153070P.
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99US-0123180P

99US-012548P

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99US-0130891P

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99US-013448P

99US-013445P

99US-013946P

99US-013946P
                                                                                                                           2000EP-00301439
                  Arabidopsis thaliana
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                                                   EP1033405-A2
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Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasorropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; Alzheimer's disease; infection; ocular disorder; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                       The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                            New protein from Neisseria gonorrheae, useful for the manufacture of medicament for treating or preventing N. gonorrheae infection.
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                                                  Masignani V, Monaci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human novel secreted protein, Seg ID 1553.
                                                                                                                                                 Disclosure; Page 666; 815pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU16600 standard; protein; 68 AA.
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50.0%; P
 12-FEB-2001; 2001GB-00003424
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2000US-0184664P.
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2000US-0205515P.
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2000US-0214886P.
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                                               Pizza M,
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                                                                         WPI; 2003-058415/05.
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Best Local Similarity
                       (CHIR-) CHIRON SPA
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16 HEFIYPDS
                                                                                      N-PSDB; ABZ40995
                                                                                                                                                                                                                                                                                     Sequence 67 AA;
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17-MAR-2000; 2
18-APR-2000; 2
19-MAY-2000; 2
07-JUN-2000; 2
30-JUN-2000; 2
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02-MAR-2000;
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990S-015822P
990S-015823P
990S-0159294P
990S-015929F
990S-015929P
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      99US-0154018P.
99US-0154039P.
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50.0%; ]
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99US-0161993P.
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IEFICLDL 47
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Best Local Similarity
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14-AUG-2000;
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29-SEP-2000;
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2000US-0241809P.
2000US-0244474P.
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2000US-024923P. 2000US-0256719P. 2000US-0251479P. 2000US-0251856P. 2000US-0251868P 2000US-0251869P 2000US-0251989P 2000US-0251990P 05-JAN-2001; 2001US-0259678P 20-OCT-2000; 2
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20-OCT-2000; 2
01-NOV-2000; 2
08-NOV-2000; 2
08-NOV 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 01-DBC-2000; 05-DBC-2000; 05-DBC-2000; 05-DBC-2000; 06-DBC-2000; 06-DBC-2000; 08-DBC-2000; 08-DBC-2000; 08-DBC-2000; 08-DBC-2000; 

Š Ruben (HUMA-) HUMAN GENOME SCI INC. Rosen CA, Barash SC,

WPI; 2001-488783/53. N-PSDB; AAS26587 New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 11; SEQ ID NO 1553; 980pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic

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immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays

(BLISA). Disorders which are diagnosed or treated include autoimmune

diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.

closedlasms of the breast or liver, cardiovascular disorders e.g. cardiac

arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,

carlest, cerebrad fungi and ocular disorders e.g. corneal infections

con also be used to aid wound healing and epithelial cell proliferation,

can also be used to aid wound healing and epithelial cell proliferation,

cto prevent skin aging due to sumburn, to maintain organs before

cransplantation, for supporting cell culture of primary tissues, to

cransplantation, for supporting cell culture of primary tissues, to

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cransplantation, for supporting cell culture of primary tissues, to

crapabilities, fat content, lipid, protein, carbohydrate, vitamins,

minerals, cofactors and other nutritional components. The present

crapabilities, fat content, lipid, protein of the invention. Note: The

sequence data for this patent did not form part of the printed
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4; Mismatches 0; Indels
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11 EEFIGGDR 18
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ABP64248 standard; protein; 68 AA. (first entry) 04-NOV-2002 Human ORF618 ABP64248; RESULT 40 ABP64248

Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary; Antiinflammatcry; gene therapy; human; ORFX; atherogenic; platelet; human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque; cancer; cardiovascular disease; allergy; autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder. 

US2002082206-A1. Homo sapiens.

27-JUN-2002.

30-MAY-2001; 2001US-00867550

30-MAY-2000; 2000US-0208427P

MEHRABAN F. CONLEY P B. TOPPER J N. LEAC/) LEACH M D. MEHR/) (CONTY)

LAW D.

(LAWD/)

ä Law Topper JN, Conley PB, Leach MD, Mehraban F,

2002-626554/67. WPI; 2002-626554/ N-PSDB; ABQ98811. New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.

Claim 10; SEQ ID NO 1236; 78pp; English.

The present invention relates to novel human ORFX polypeptides and their coding sequences (ABP63631-ABP64681 and ABQ98194-ABQ99267). The sequences

2000US-0229345P

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data
were discovered in human atherogenic cells, in particular in platelets and human unbilical vein endothelial cells (HUVEC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherosclerotic plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological condition associated with an ORFX associated disorder, e.g. canner, cardiovascular disease, allergy, autoimmune disease, wound healing, bloo coagulation disorders or inflammatory disorders. Note: The sequence data for this patent did not form part of the printed specification, but was segdata.uspto.gov/sequence.html?bocID=20020082206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; neural disorder; immune system disorder; renal disorder; muscular disorder; disorder; disorder; disorder; pulmonary disorder; cardiovascular disorder; pulmonary disorder; cardiovascular disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiatlergic; thrombolytic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0225757P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0225758P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
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Best Local Similarity
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21 CEFIKGDK
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                                                                                                                                                                                                                                                                                                                                                 Sequence 68 AA;
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07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2000;
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14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU55669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 41
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5' EST; expressed sequence tag; secreted protein; cDNA isolation;

Human secreted protein, SEQ ID NO: 5197.

(first entry)

06-OCT-2000

AAG01116;

gene therapy; chromosome mapping

Homo sapiens EP1033401-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. system; lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left (e.g. congenital heart defects, e.g. acute kidney failure and end stage creal disease), hyperproliferative disorders (e.g. Hodgkin's disease and clenkaemia), inflammatory diseases (e.g. septic shock, bursitis and spendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and ABUS5748 represent human novel polypeptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 1553; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barash SC;
                                                              2000US-0234223P.
2000US-0234274P.
2000US-023423P.
2000US-0235834P.
2000US-023537P.
2000US-023537P.
2000US-023538P.
2000US-023538P.
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2000US-023538P.
2000US-023538P.
2000US-023538P.
2000US-023538P.
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2000US-0240960P.
2000US-0241785P.
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2000US-0244617P.
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2000US-0251856P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2003-147444/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROSEN C A. RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABX73928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  renal disorders.
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                                                                                                                                                                                                                                                           02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
03-0CT-2000;
03-0C
                                                                                                                                                      29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 2
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29-SEP-2000;
                                                                                                           25-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000;
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                                                                                         21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-2000;
                                                                   21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ROSE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RUBE/)
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New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.

Giordano J;

Duclert A,

Dumas Milne Edwards J,

26-FEB-1999; (GEST ) GENSET WPI; 2000-500381/45.

N-PSDB; AAC01122

21-FEB-2000; 2000EP-00200610.

36-SEP-2000.

99US-0122487P.

claim 13; SEQ ID NO 5197; 71pp + Sequence Listing; English.

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0
The present sequence is a polypeptide encoded by one of a large number of 5. ESTB derived from mRNAs encoding secreted proteins. The 5. ESTB were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3. untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTB are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTB are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTB
                                                                                                                                                                                                                                                                are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 3; Length 69; 50.0%; Pred. No. 1.1e+03; cive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibacterial; infection; vaccine; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N. gonorrhoeae amino acid sequence SEQ ID 1906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.1e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP77688 standard; protein; 69 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria gonorrhoeae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||::|:
32 VEFIRHDR 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 XEFIXXDX 8
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 69 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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AAG01116 standard; protein; 69 AA.

RESULT 42 AAG01116

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1 XEFIXXDX 8

8 6

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Gaps

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Length 72; Indels

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61 QEFIGNDR 68
                                                                                                                                                                                                                                                      (HYBR-) HYBRIGENICS.
(INSP ) INST PASTEUR
                                            WPI; 2003-058415/05
                                                                                                                                         1 XEFIXXDX 8
                                                                                                                                                                                                              Helicobacter pylori
                                                                                                                                                                                                                                                                    Legrain P, Rain J,
                                                                                                                                                                                                                                                                           WPI; 2002-674910/72.
N-PSDB; ABX66637.
                                                                                                                        Query Match
Best Local Similarity
                            (CHIR-) CHIRON SPA
                                                N-PSDB; ABZ38658.
                                                                                                                 Sequence 69 AA;
                                                                                                                                                                                                                      WO200266501-A2.
                                    Fontana MR,
    10-OCT-2002.
                                                                                                                                                                                      07-MAY-2003
                                                                                                                                 4 ;
                                                                                                                                                                                                                               29-AUG-2002.
                                                                                                                                                                              ABU51892;
                                                                                                                                 Matches
                                                                                                                                                              RESULT 44
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The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID), identified via protein-protein interactions. Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes substantially purified human proteins (referred to as open reading frame, OREX, where X is 1.11491 (see Tabl in the specification). ABN15762 to ABN2752 encode the human OREX proteins given in ABP00010 to ABP11500. OREX proteins are useful for treating or preventing a pathology associated with an OREX-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 5; L
Pred. No. 1.1e+03;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ORFX protein sequence SEQ ID NO:18836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, SEQ ID NO 18836, 1037pp, English.
Claim 6; Page 386; 642pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 AA.
                                                                                                                                                                                                                                                                 represent an illegible residue
                                                                                                                                                                                                                                                                                                                                                        100.08;
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29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                          50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP09427 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEFIYADN 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-106308/14.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABN25179
                                                                                                                                                                                                                                                                                                            Sequence 72 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 45
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                                                                                                                                                                                                                                                                                                                                                                                                                               Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                                                                                                                                                                                                              New protein from Neisseria gonorrheae, useful for the manufacture of a medicament for treating or preventing N. gonorrheae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to proteins from Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein-protein interaction; ulcer; selected interacting domain; SID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori selected interacting domain (SID) protein #1236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
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Pred. No. 1.1e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Labigne A;
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                                                                                                                                                                                       Masignani V, Monaci
                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 325, 815pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU51892 standard; protein; 72 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
50.0%; P
                                                    12-FEB-2002; 2002WO-IB002069.
                                                                                                  12-FEB-2001; 2001GB-00003424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-2001; 2001WO-EP015428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JAN-2001; 2001US-0259302P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                       Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ulcers in mammals
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(see Table 1

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Screening for non-ocular disease - by analysing tears for marker proteins, particularly indicative of cancer and genetic disease, also new proteins and nucleic acid encoding them.
disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with OREX-associated disorder. OREX polymuclectide sequences can be used in pene therapy. OREX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, Reloid, degenerative disorders, haemorrhage, osteoarthriis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic tupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple solerois, rhematoid
                                                                                                                                                                                                arthritis, autoimmune thyroidis, myasthenia gravis, graft-versus-host disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerating disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The markers AAW61647-W61649 are used for screening for, or detecting, non-ocular disease by analysing tears. Biochemicals, specifically proteins, are isolated from tears, particularly by chromatography or electrophoresis, especially two-dimensional polyacrylamide gel electrophoresis (2D-PAGB), then detected, e.g. with labelled specific reagents, in (radio)immunoassay. The method is used to detect cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                , Score 25; DB 5; Length 73; Pred. No. 1.2e+03; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; non-ocular disease; tear; cancer; breast; prostate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herbert B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walsh B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW61649 standard; peptide; 74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bolis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 9; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-AU000011.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-ocular disease marker 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MACQ-) MACQUARIE RES LTD. (UNIX ) UNISEARCH LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Willcox M, Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-447373/38.
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2 LEFIPSDQ 9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9835229-A1
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Gooley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                 epidermidis; open reading frame; ORF; bacterial infection;
particularly of breast or prostate, or a genetic disease, in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3004.
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                                                                           ; Score 25; DB 2; Length 74
Pred. No. 1.2e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 3004; 267pp; English
                                                                                                                                                                                                                                                 ABP38159 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOME THERAPEUTICS CORP.
                                                                            100.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00134001.
                                                                                                                                                                                                                                                                                                                                                                                        gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                              4; Conservative
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QEFIDSDA 36
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                                                                                                                                         1 XEFIXXDX 8
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Matches 4; Conserv
                                                                              Query Match
Best Local Similarity
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                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                         antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6380370-B1
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                                                   74
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                                                   Sequence
                    animals
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ID ABP3
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Molloy M;

48

RESULT

1 XEFIXXDX 8

Page 31

ADA36717

us-09-660-302e-1.rag

Lonetto MA, Nicholas RO;

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Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that of a Streptococcal polypeptide. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypethyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 2; Length 82;
Pred. No. 1.3e+03;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ORFX protein sequence SEQ ID NO:17204.
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4, Mismatches
                                                                                                                                                                                             Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP08611 standard; protein; 82 AA.
                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 40; 181pp; English.
                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
50.0%; F
                                                          97WO-US021976.
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29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                         Black MT, Hodgson JE,
Reid RH, Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                    WPI; 1998-322654/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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58 NEFIALDD
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                                                                                                                                                                                                                                                                        N-PSDB; AAV42950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 82 AA;
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                                                        24-NOV-1997;
                                                                                              27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                    04-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-2002
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Matches
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated Acinetobacter baumannii nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                   Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 25; DB 6; Length 80; Pred. No. 1.3e+03; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; SEQ ID NO 8004; 328pp; English
                                                                                                                             Acinetobacter baumannii protein #3878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae polypeptide.
            ADA36717 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW62670 standard; protein; 82 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                          Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 DEFIFKDK 37
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      baumannii protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-576092/
N-PSDB; ADA32591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 80 AA;
                                                                                                                                                                                                                                                                                                                                             04-JUN-1999;
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                                                                                        20-NOV-2003
                                                                                                                                                                                                                                                                                                       13-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Breton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW62670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plants.
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Gaps

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Leach MD;

Shimkets RA,

(CURA-) CURAGEN CORP.

Streptococcus pneumoniae

ò g WO9823631-A1

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The present invention describes substantially purified human proteins

(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABD0010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX associated disorder. ORFX polymucleotide squences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arbitis, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoprosis, bone degenerative disorders, or periodontal disease, and for gut reading virture, in various reader to reading osteoprosis, constitution in the profession or reading osteoprosis, constitution in the profession or periodontal disease, and for gut reading or injury, in various end treatment of lung or liver form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aminoacyl-tRNA synthetase; isoleucyl-tRNA synthetase; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lysyl-tRNA synthetase; phenylalanyl-tRNA synthetase; gene expression;
prolyl-tRNA synthetase; herbicide identification; genetic marker;
plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                            Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 5; Length 82; 50.0%; Pred. No. 1.3e+03; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice isoleucyl-RNA synthetase protein sequence.
                                                                                                                                                                    Disclosure; SEQ ID NO 17204; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "encoded by NGG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB83324 standard; protein; 83 AA.
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62 REFICIDT 69
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Best Local Similarity
4; Conserve
               WPI; 2002-106308/14.
N-PSDB; ABN24363.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 82 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-1999;
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This sequence is a plant aminoacyl-tRNA synthetase of the invention. The aminoacyl-tRNA synthetases are selected from isoleucyl-tRNA synthetase, ipenylalanyl-tRNA synthetase, phenylalanyl-tRNA synthetase, and prolyl-tRNA synthetase, phenylalanyl-tRNA synthetase, and prolyl-tRNA synthetase. The nucleic acid fragments may be used to create transgenic plants in which the polypeptides are present at higher or lower levels than normally found. This would have the effect of altering the level of aminoacyl-tRNA synthetase activity and gene expression in those cells. The polypeptides can be used as a targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. All or a substantial portion of the nucleic acid fragments may also be used as probes for genetically and physically mapping the genes. Such information may be useful in plant breeding in order to chose genes. Such information may be useful in plant breeding in order to
                                                                                                                                           Isolated polynuclectide encoding plant isolewcyl-tRNA synthase, useful for creating transgenic plants and as targets to facilitate design and/or identification of inhibitors that may be useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice; isoleucyl-tRNA synthetase; lysyl-tRNA synthetase; phenylalanyl-tRNA synthetase; prolyl-tRNA synthetase; aminoacyl-tRNA synthetase; herbicide; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rice isoleucy1-tRNA synthetase clone rls2.pk0006.c10.
                                                               Orozco EM, Schwaber JS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU08739 standard; protein; 83 AA.
                                                                                                                                                                                                              Claim 1; Col 25-28; 50pp; English
                                (DUPO ) DU PONT DE NEMOURS & CO
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50.0%; F
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99US-00357251.
98US-0093530P
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Best Local Similarity 50.0.
                                                                Famodu LO,
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31 EEFIFYDG 38
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                                                                                               WPI; 2001-482449/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 76
                                                                                                                N-PSDB; AAF87079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 83 AA;
 21-JUL-1998;
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20-JUL-1999;
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                                                                Falco SC,
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9905-0139817P

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9905-0140635P

9905-0140823P

9905-014081P

9905-014283P

9905-014283P

9905-014283P

9905-014283P

9905-014488P

9905-014488P

9905-014408P

9905-014408P
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990S-013943P
990S-0139454P
990S-0139455P
990S-0139457P
990S-0139458P
990S-0139458P
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99US-0136392P.
99US-0136782P.
99US-0137222P.
                                                             99US-0132486P.
99US-0132487P.
99US-0132863P.
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99US-0134219P.
99US-0134221P.
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99US-0135353P.
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                   99US-0132048P.
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99US-0137502P.
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                  30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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25 - MAY - 1
27 - MAY - 1
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04-JUN-
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19-MAY-
20-MAY-
21-MAY-
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14-MAY-
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                                                                                              11-MAY
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isolencyl-tena synthetase, a lysyl-tena synthetase, a phenylalanyl-tena synthetase, or a prolyl-tena synthetase. The nucleic acid fragments encoding aminoacyl-tena synthetases are useful in developing new herbicides that target aminoacyl-tena synthetases and engineer aminoacyl-tena synthetases and engineer aminoacyl-tena synthetases and engineer aminoacyl-tena synthetases that are resistant to the herbicides. The nucleic acid profesion synthesis in plants, providing studies to better understand protein synthesis in plants, providing genetic tools for the manipulation of gene expression, or providing possible target for herbicides. The polypeptides are useful as targets to facilitate design and/or identification of inhibitors of the aminoacyl-tena synthetases that may be used as herbicides. This is the aminoacyl-tena synthetases that may be used as herbicides. This is the amino acid sequence of rice isoleucyl-tena synthetase clone rls2.pk0006.clo
                                                                        New nucleic acid fragments encoding aminoacyl-tRNA synthetases, useful in developing new herbicides that target aminoacyl-tRNA synthetases and engineer aminoacyl-tRNA synthetases that are resistant to the herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                       The invention describes an isolated nucleic acid fragment encoding an
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 6; Length 83; 50.0%; Pred. No. 1.3e+03; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 20148.
                     Simmons CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG18654 standard; protein; 85 AA
                                                                                                                    Claim 6; Page 15; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0121825P.
99US-0123180P.
99US-0125788P.
99US-012678P.
99US-0126785P.
99US-0128234P.
99US-0128234P.
99US-0130774P.
99US-013047P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                         4; Conservative
                     Falco SC, Famodu 00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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31 EEFIFYDG 38
(SIMM/) SIMMONS C R.
                                         WPI; 2003-401721/38.
N-PSDB; ABX95455.
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                               Sequence 83 AA;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
116-APR-1999;
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9905-01473039

9905-0147416P

9905-01474318P

9905-0148171P

9905-014864P

9905-014864P

9905-014864P

9905-0149642F

9905-014972B

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9905-014972B

9905-0149902P

9905-0149902P

9905-0149902P

9905-0149902P

9905-0149930P

9905-015066F

9905-0151066P

9905-015108P

9905-015108P
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9905-0159293P
9905-0159294P
9905-0159330P
9905-0159331P
9905-0159331P
                                                  990S-0145088P.
990S-0145085P.
990S-0145087P.
990S-0145192P.
990S-0145192P.
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99US - 01452769.
99US - 0145913P.
99US - 0145919P.
99US - 0145919P.
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99US-0146389P.
99US-0147038P.
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99US-0147302P.
99US-0147192P.
99US-0147260P.
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04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
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13-AUG-1999;

16-AUG-1999;

18-AUG-1999;

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25-AUG-1999;

26-AUG-1999;
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11-AUG-1999;
12-AUG-1999;
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31-AUG-1999;
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02-AUG-1999
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The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an B-value greater by a factor of 3 than the B-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herbicidally active polypeptide SEQ ID NO 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                         ABB90813 standard; protein; 89 AA
         9905-0159584P-
9905-0160741P-
9905-016076P-
9905-016070P-
9905-0160814P-
9905-0160981P-
9905-0160981P-
9905-0160981P-
9905-0161406P-
9905-0161406P-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                4; Conservative
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13 PEFIFEDG 20
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                                                                                                                                                                                                                                                                                                                        1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200210210-A2.
          18-0CT-1999
21-0CT-1999
21-0CT-1999
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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                           Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 15438; 1037pp; English.
                                                                                      Human ORFX protein sequence SEQ ID NO:15438.
                      ABP07728 standard; protein; 94 AA.
                                                                                                                                                                                                                                                                              29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                 30-MAY-2000; 2000US-0206132P.
                                                                                                                                                                                                                                                                                                             29-AUG-2000; 2000US-0228716P.
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                        Leach
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-106308/14.
                                                                                                                                                                                         myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABN23480.
                                                                                                                                                                                                                                  WO200192523-A2.
                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                         Shimkets RA,
                                                                 25-JUN-2002
                                                                                                                                                                                                                                                        06-DEC-2001
                                            ABP07728;
                                                                                                                                                                                                              Homo
RESULT 56
                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human relaxin may be prepd. by combining the A and B chains of relaxin in full-length, shortened or modified forms. Prefd. analogues consist of any one of the A-chains A(1-24), A(2-24), A(3-24) in combination with any of the B-chains B(1-23) to B(1-32). (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uman relaxin analogues - has shortened and/or modified forms of natural and/or A chains modified by addn. of protective gp. to free amino gp.
                                                                            Gaps
  identifying modulators. The identified modulators are useful as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 90;
                                                        Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 25; DB 1; Length 90
Pred. No. 1.4e+03;
4; Mismatches 0; Indels
                                            Score 25; DB 5,
-4 No. 1.4e+03; 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tregear GW;
                                                                 Pred. No. 1.4e
4; Mismatches
                                                                                                                                                                                                                                                                              Hormone; relaxin analogue; antagonist
                                                                                                                                                                                                                                                        Sequence of human prorelaxin B chain.
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2B; 22pp; English.
                                                                                                                                                                             AAP81887 standard; protein; 90 AA
                                                                                                                                                                                                                                                                                                                                                                    /label= C PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Niall HD,
                                                                                                                                                                                                                                                                                                                                              'label= B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                     83EP-00104503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          82AU-00005352.
88EP-00104503.
                                                         100.0%;
                                                                 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FLOR-) FLOREY INST EXP PHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.00,
                                                                                                                                                                                                                                    (first entry)
                                                                              Conservative
                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shine J,
                                                                                                              :|||::|:
52 TEFIRSDI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1988-300910/43.
                                                                                                  1 XEFIXXDX 8
                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN81773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 90 AA;
                                   Sequence 89 AA;
                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     11-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-1982;
23-APR-1987;
                                                                                                                                                                                                                                 31-DEC-1990
                                                                               4;
                                                                                                                                                                                                                         25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                          EP287820-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hudson PJ,
             herbicides
                                                                                                                                                                                                   AAP81887;
                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                     Region
                                                                               Matches
                                                                                                                                                                  RESULT
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The present invention describes substantially purified human proteins

(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX in the specification). ABN15762 to ABN27252 encode the human ORFX in the specification). ABN15762 to ABN27252 encode the human ORFX is considered to proteins given in ABD0010 to ABN12700. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX associated disorder. ORFX polynucleotide squences can be used in Gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoathritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertrension, hypothyroidism, cholesterol ester storage disease, autoimmune disorders such as multiple sclerosis, rheumatoid atthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        form part of the printed specification, but was obtained in electional format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 1.5e+03;
4; Mismatches 0;
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Best Local Similarity 50.0%;
Matches 4; Conservative 4
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Gaps

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50.0%;

29 QEFINKDT 36

1 XEFIXXDX 8

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1 XEFIXXDX

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This sequence comprises human endometrial specific steroid binding factor III (ESF III), a protein that inhibits phospholipase A2 activity, binds to polychlorinated biphenyl compounds, reduces foreign protein antigenicity, inhibits monocyte and neutrophil chemotaxis and phagocytosis, inhibits monocyte and neutrophil chemotaxis and controls the growth of endometrial cells. The amino acid sequence was deduced from a CDM clone (see AAT94832) derived from a human endometrial tumour. ESF I (see AAW35802) and ESF II (see AAW35802) and ESF II (see CAW35803) are also claimed. Human ESF III has about 36% identity with rat prostatic steroid-binding protein. Recombinant ESF I, II and III can be expressed in host cells for use in claimed methods (a) for treating a patient in need of ESF I, II or III (including expression of the patient in need of ESF I II or III (including expression of the compounds which bind to and inhibit activation of the ESF polypeptide. HESF I, II and III may be used to the treating a compounds which the Library compounds which thind the contraction of the ESF polypeptide. HESF I, II and III may be used to the test inflammation, asthma, rhinitis, cystic fibrosis, airway disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endometrial specific steroid-binding factor III; ESF III; human; Clara cell secretory protein; endometrium; phospholipase A2 inhibitor; polychlorinated biphenyl; antiaggregant; inflammation; asthma; rhinitis; cystic fibrosis; airway disease; neoplasia; atopy; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human endometrial specific steroid-binding factor I, II and III - used
treat inflammation, asthma, rhinitis, cystic fibrosis, airway disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human endometrial specific steroid-binding factor III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .21
/label= Sig_peptide
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/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                          AAW35804 standard; protein; 95 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US003857.
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neoplasia, atopy etc.
                                                                 47 PEFIEVDL 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neoplasia and atopy
XEFIXXDX
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                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9734997-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-1997.
                                                                                                                                                                                                                                                                                                                                AAW35804;
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                                                                                                                                                                                 RESULT 57
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and quantitate gene expression in biopsied tissues. With respect to cancer a relatively high amount of transcript may indicate a predisposition for the development of disease. The nucleic acid sequences which encode HWH may also be used to generate hybridization probes useful for mapping the naturally occurring genomic sequence. HMH, and its fragments/variants can be used for screening libraries of compounds in drug screening techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human mammoglobin homologue (HWH). Antagonists of the HMH polypeptide can be used to treat neoplastic disorders including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma and teratocarcinoma. A vector expressing the complement of the polynucleotide encoding HMH may be administered to a subject to treat or prevent neoplastic disorders or endometriosis. Antibodies which bind HMH may also be used in the diagnosis of conditions or diseases characterized by expression of HMH, or in assays to monitor patients being treated with HMH, agonists, antagonists or inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human mammoglobin homolog (HMH), useful for diagnosing, treating or preventing disorders associated with expression of HMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                 Human manmoglobin homologue, HMH; antagonist; neoplastic disorder;
adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma;
teratocarcinoma; endometriosis.
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50.0%; Pred. No. 1.5e+03;
ive 4; Mismatches 0; Indels
                                                                                                                                                                                                 A human mammoglobin homologue (HMH).
                                                                                                AAY02590 standard; protein; 95 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1A-B; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murry LE;
                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US021729.
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                                                                                                                                                                  (first entry)
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Matches 4; Conservative
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47 QEFIDSDA 54
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                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                    WO9919487-A1
                                                                                                                                                                                                                                                                                                                                                                                                      14-OCT-1998;
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                                                                                                                                                                  26-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                       22-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillman JL,
                                                                                                                                  AAY02590;
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ID AAB0
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Gaps

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100.0%; Score 25; DB 2; Length 95; llarity 50.0%; Pred. No. 1.5e+03; Conservative 4; Mismatches 0; Indels

Best Local Similarity Matches 4: Conserve

Query Match

(first entry)

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This invention relates to nucleic acid molecules encoding portions of the human endometrial specific steroid-binding factors I, II, and III. Also included in the invention are hESF I, II, and III polypeptides sequences. The included in the invention are hESF I, II, and III polypeptides sequences. The included in the invention are hESF I, III and III polypeptides are used in gene therapy to express hESF I, II and III polypeptides in vivo to treat and/or prevent inflammation, asthma, rhinitis, cystic fibrosis, air way disease, neoplasia and actory. The polymuclectides are also used to inhibit phospholipase A2 activity, bind polychorinate binded biphenyls, reduce foreign protein antigate, inhibit monocyte and neutrophil chemotaxis and phagocytosis, inhibit platelet aggregation, regulate elossanoid cand phagocytosis, inhibit platelet aggregation, regulate elossanoid conceptions in the human uterus and control the growth of endometrial cells. The polymucleotides are also useful for detecting complementary polymucleotides are used to detect complementary polymucleotides such a disgnostic reagent. The hESF I, II and III associated with a dysfunction will provide a diagnostic tool that can define diagnosis of a disease or susceptibility to a disease which can mador-expression, over-expression of an endometrial cancer. They are also useful for chromosome identification.

The present sequence represents a hESF III protein sequence identified in
                                                                                                                                   Endometrial specific steroid-binding factor; human; hESF; inflammation; asthma; rhinitis; cystic fibrosis; air way disease; neoplasia; atopy; eicosanoid level regulator; chemotaxis inhibitor; endometrial cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel gene encoding human endometrial specific steroid-binding factor I, II and III which is useful for treating asthma, rhinitis, cystic fibrosis, airway disease and neoplasia.
                                                                                           Human endometrial specific steroid-binding factor III protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 3; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gentz R, Ni J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-375600/32.
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Best Local Similarity
Matches 4; Conserv
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                                                       06-OCT-2000
                                                                                                                                                                                                                                                                                                                                            21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-1996;
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                            US6066724-A
                                                                                                                                                                                                                                                                                                    23-MAY-2000
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                   AAB03769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yu G,
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96US-0014724P. 97US-00821451.

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represent the EST-related proteins corresponding to AAX65651 to AAX65438

Crepresent the EST-related proteins corresponding to AAX42665 to AAX43052.

The 5' BSTs can be used for producing screted human gene products. They

can be used to identify and isolate 5' untranslated regions (UTRS) and

cupstream regulatory regions which control the location, development

creptage, rate, and quantity of protein synthesis, as well as stability of

mANA. The ESTs are also useful as probes for chromosome mapping, and to

chain full length cDNA clones. The ESTs can also be used in forensic

contain full length cDNA clones. The ESTs can also be used in forensic

contain full september of identify individuals, or in diagnostic procedures to

cidentify individuals paring genetic diseases resulting from abnormal gene

expression. The products may also be used in gene therapy protocols. The

concleic acids encoding signal peptides can be used for directing

extracellular secretion of a polypeptide or the insertion of a

colypeptide into a membrane, or importing a polypeptide into a cell. The

proteins encoded by the EST sequences may be useful in treating a variety

colf human conditions. Secreted proteins have therapeutic value, and the

colf human conditions respected proteins is valuable. AAZ42249 to AAZ42264

colf human conditions represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                        Human, 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tag sequences used in
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                                                                     Human 5' EST related polypeptide SEQ ID NO:1555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 818; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY92226 standard; protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08;
                                                                                                                                                                                                                                                                                                                                  99WO-IB000712.
                                                                                                                                                                                                                                                                                                                                                                     98US-00057719.
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                                    01-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||::|:
QEFIDSDA 54
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                     location; deve
                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                     W09953051-A2.
                                                                                                                                                                                                                                                                                                                                  09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                         09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                            28-APR-1998;
                                                                                                                                                                                                                                                                                            21-OCT-1999
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AAY65394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 61
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Gaps 0;

100.0%; Score 25; DB 3; Length 95; 50.0%; Pred. No. 1.5e+03; ive 4; Mismatches 0; Indels

Conservative

OEFIDSDA

AAY65394 standard; protein; 95 AA.

RESULT 60 AAY65394 ID AAY65 XX

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Clone Mamm-X encodes a polypeptide that is 100 pecent identical to human Mammaglobin B precursor, a potential marker of breast cancer nodal metastasis. The sequences are useful for treatment of diseases such as cancer, immune disorders, autoimmune disease, acquired immune deficiency syndrome (AIDS) transplant rejection, allergy, infection by a pathological agent or organism, inflammatory disorders, arthritis, a haematopoietic disorder, a skin disorder, atherosclerosis, restenosis, a neurological disease, Alzheimer's disease, trauma, spinal cord injury and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; endometrial specific steroid binding factor; hESF; hESF1; hESF11; hESF11; inflammation; asthma; rhinitis; cystic fibrosis; airway disease; neoplasia; atopy; phospholipase A2; polychlorinated biphenyl; chemotaxis; phagocytosis; platelet aggregation; eicosanoid; endometrial cell.
                                                                                                                                                                                              Nucleic acids encoding polypeptides with syncline-like, claudin-like or cytokine-like activity, useful for treating diseases including cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human endometrial specific steroid binding factors, useful for treating and preventing inflammation, asthma, rhinitis, cystic fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 3; Length 95
Pred. No. 1.5e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An endometrial specific steroid binding factor III.
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/note= "signal peptide"
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                                                                                                                                                                                                                                                           Alzheimer's and atherosclerosis.
                                                                                                                                                                                                                                                                                                                     Claim 23; Fig 6; 118pp; English
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50.0%; Pre
tive 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB31682 standard; protein; 95
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97US-00821451.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                2000-303741/26.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 QEFIDSDA
                                                                                                                                        N-PSDB; AAA09118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN
                                                      Shimkets RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6174992-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB31682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The levels of human endometrial specific steroid binding factor (ESBPIII) can be measured and compared to control levels and used to diagnose the presence of a gynaecological (uterine, breast, endometrial, or ovarian) cancer in a patient. ESBPIII levels can also be used to diagnose metastasis, to stage or monitor gynaecological cancer. Antibodies specific for ESBPIII can be used to treat gynecological cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    staging and monitoring gynecological cancer comprising using level of ESBPIII in a patient as an indicator of cancer.
                                                                  Endometrial specific steroid binding factor, ESBPIII, diagnosis,
gynaecological cancer, uterine, breast, endometrial, ovarian, antibody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone Mamm-X; mammaglobin; breast cancer; cytostatic; anti-HIV; mimunosuppressive; antiallergic; antiinfective; antiinflammatory; antiarthritic; antiateriosclerotic; vasotropic; neuroprotective; nootropic; dermatological; tranquilizer; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 3; Length 95; 50.0%; Pred. No. 1.5e+03; 1.ve 4; Mismatches 0; Indels
            Human endometrial specific steroid binding factor III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 28-29; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                  99WO-US022753
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99US-00412231
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                                                                                                                               gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DIAD-) DIADEXUS LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-303649/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 AA;
                                                                                                                                                                                                                                            WO200020044-A1
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                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing,
an elevated
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05-OCT-1999;
                                                                                                                                                                                                                                                                                                         13-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macina RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S:
Matches 4,
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Length 95;

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                                                     The present sequence represents a human endometrial specific steroid hinding factor (hESF). The specification describes hESF1, hESFI1, and hESFIII. I and III polypeptides, and polymucleotides encoding them are useful for treating and preventing inflammation, asthma, inhibiting phospholipase A2 activity, binding polychlorinated biphenyls, reducing foreign protein antigencity, inhibiting monoryte and neutrophil chemotaxis and phagocytosis, inhibiting platelet aggregation, regulating chosping in the human uterus, and for controlling the growth of endometrial cells. hESF polypeptides and nucleotides are also useful for research, biological, clinical or therapeutic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides having the sequence of human lipophilin A, B and C are associated with carcinomas of hormonally regulated organs and are useful in the diagnosis and prognosis of various cancers.
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic epitope; hormonally regulated organ; malignant tumour; Lipophilin; human.
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0
                                                                                                                                                                                                                                                                              Length 95;
                                                                                                                                                                                                                                                                             Score 25; DB 4; Length 95
Pred. No. 1.5e+03;
4; Mismatches 0; Indels
 airway disease, neoplasia and atopy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Fig 6; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein of human Lipophilin C.
                                                                                                                                                                                                                                                                              100.0%;
                                Claim 1; Fig 3; 36pp; English
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                                                                                                                                                                                                                                                                                                             Conservative
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OEFIDSDA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLASGOW B J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-338922/37
                                                                                                                                                                                                                                                                                                                                            1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LEHR/) LEHRER R I.
                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2002034739-A1.
                                                                                                                                                                                                                                                 Sequence 95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZHAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-1998;
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                                                                                                                                                                                                                                                                                                          4,
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                                                                                                                                                                                                                                                                                                                                                                         47
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                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        64
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                                                                                                                                                                                                                                                                                                                                   Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kovatis SG;
, Mills GB;
                                                             0
                           Length 95;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gannavarapu M, Hoersch S, Kamatkar S, Ko
Morrisey MP, Olandt PJ, Sen A, Vieby PO,
1 K, Schmandt RE, Zhao X, Glatt K;
                           ; Score 25; DB 5; L. Pred. No. 1.5e+03; 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 303; 481pp; English.
                                                                                                                                                                                                            95 AA
                                                                                                                                                                                                                                                                                                           Human ovarian cancer marker M458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-0276025P.
2001US-0311722P.
2001US-031380P.
2001US-0324967P.
2001US-0325102P.
                            100.0%;
50.0%; F
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                                                                                                                                                                                                            ABG96366 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from a non cancer patient.
                                                                                                                                                                                                                                                                           (first entry)
                                                               Conservative
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N-PSDB; ABS76462.
                                                                                                                            54
                              Query Match
Best Local Similarity
                                                                                                                :|||::|:
47 QEFIDSDA
                                                                                             1 XEFIXXDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lu K,
Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200271928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-2001;
14-MAR-2001;
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26-SEP-2001;
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Bast RC,
                                                                                                                                                                                                                                            ABG96366;
                                                             Matches
                                                                                                                                                                               RESULT 65
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testicular disorders (e.g. nontuberculous granulomatcus orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present amino acid sequence represents one of the ovarian cancer markers described in the
           of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibody specific for human endometrial specific steroid-binding factor (hESF) III, useful for detecting hESF III protein in biological sample and to isolate or identify clones expressing the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, endometrial specific steroid-binding factor; BSF;
prostatic steroid-binding protein; hBSF I; hBSF II; hBSF III; asthma.
                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human endometrial specific steroid-binding factor (hESF) III.
                                                                                                                                                                                                                                                                                                    Score 25; DB 5; Length 95;
Pred. No. 1.5e+03;
4; Mismatches 0; Indels
The cancer markers may be used in the
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/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
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                                                                                                                                                                                                                                                                                                                                       4;
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                                                                                                                                                                                                                                                                                                    100.0%;
50.0%; F
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99US-00263810.
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                                                                                                                                                                                                                                                                                                                                       4; Conservative
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QEFIDSDA 54
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Atches 4; Conservance
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                                                                                                                                                                                                                                                                         Sequence 95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-1996;
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08-MAR-1999;
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                                                                                                                                                                                                                                           Invention
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The present sequence represents a endometrial specific steroid-binding

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factor (hESF) III. The full length protein has a molecular weight of 8.10 KDB. The protein has homology to rat prostatic steroid-binding protein C3. Antibodies which bind hESF proteins, such as hESF I, hESF II, and hESF III are useful for isolating or to identify clones expressing the bolypeptides or to purify the polypeptides by affinity chromatography. Agonists and antagonists of hESF proteins are useful for treating and/or preventing susceptibility to asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endometrial specific steroid-binding factors 1, II and III (HESF I, II and III), and the nucleic acids encoding them. The HESF polypeptide has homologies to mammalian Clara cell 10 kba (CCIO) secretory protein and rat prostatic steroid-binding protein which are factors which modulate or mediate the action of hormones involved in the regulation of functions of the lung and uterus. The nucleic acids and polypeptides can be used to identify compounds that bind to and inhibit activation, raise antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endometrial specific steroid-binding factor (hBSF) proteins and sful for treating or diagnosing a disease or susceptibility to a
                                                                                                                                                                                                                                                                                                                                                                                                                   Human endometrial specific steroid-binding factor III (hESF III) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, endometrial specific steroid-binding factor; hESF;
Clara cell 10 kDa, CC10; secretory protein; asthma;
prostatic steroid-binding protein; hormone; lung; uterus; gene therapy.
                                                                                                                                                                                         Gaps
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                                                                                                                                                                                        .
                                                                                                                                                         Length 95;
                                                                                                                                                                                      Indels
                                                                                                                                                        Score 25; DB 5; L
Pred. No. 1.5e+03;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .21
|label= Signal_peptide
| 2. .95
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97US-00821451.
99US-00263810.
                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease, particularly asthma.
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                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                   Local Similarity 50.0 les 4; Conservative
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OEFIDSDA 54
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                                                                                                                            AA;
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                                                                                                                           Sequence 95
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                                                                                                                                                      Query Match
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                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression
or develop antagonists against the isolated hESF polypeptide. The polypeptides or polymuclectides are useful for treating a patient having a need of hESF I, hESF II, hESF III or for treating a patient having a need to inhibit hESF. The polypeptide is administered by providing to the patient the DNA encoding the hESF polypeptide in vivo (gene therapy). In paticular, the disease is asthma. The hESF polypeptides or polymuclectides are also useful for diagnosing a disease or a susceptibility to the disease. The sequence presented is the hESF III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meyers RE;
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers R
Bast RC, Hortobagyi GN, Pusztai L, Meric P, Sahin A, Mills GB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breast cancer diagnosis or treatment by comparing the level of expriof a marker in a patient sample with that in the control non-breast cancer sample.
                                                                                                                                                                                        0;
                                                                                                                                                            Score 25; DB 6; Length 95
Pred. No. 1.5e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Breast cancer associated protein sequence SEQ ID NO:280.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; breast cancer; cytostatic; gene therapy
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                                                                                                                                                                                                                                                                                                            ABR47522 standard; protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-2001; 2001US-0299887P.
27-JUN-2001; 2001US-0301572P.
18-JUL-2001; 2001US-0306501P.
25-SEP-2001; 2001US-0362502P.
05-MAR-2002; 2002US-0362585P.
                                                                                                                                                               100.08;
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                                                                                                                                                                        50.0%;
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les 4; Conservative
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QEFIDSDA 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003004989-A2
                                                                                                                                      Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PRO polynucleotide and polypeptide, useful for the manufacture of a medicament for diagnosing or treating cancer or inflammatory bowel disorder e.g., ulcerative colitis or Crohn's disease.
N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; PRO; cancer; inflammatory bowel disease; ulcerative colitis; Crohn's disease.
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Pred. No. 1.5e+03;
4; Mismatches 0; Indels
                                                                                                                                    Length 95;
                                                                                                                                                                               Indels
                                                                                                                                  ; Score 25; DB 6; L. Pred. No. 1.5e+03; 4; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                  ADC78795 standard; protein; 95 AA.
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50.0%; E
                                                                                                                                      100.08;
50.08; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-2002; 2002WO-US033070.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO protein #12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-481990/45.
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QEFIDSDA 54
                                                                                                                                                                                                                                                                    54
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                                                                                                                                                           Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                      : | | | :: | :
47 QEFIDSDA
                                                                                                                                                                                                                             1 XEFIXXDX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 95 AA;
                                                                                             Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                           ADC78795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 70
                                                                                                                                                                                                                                                                                                                                    RESULT 69
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myasthenia gravís.
                                                       WPI; 2002-106308/
N-PSDB; ABN17338.
                              WO200192523-A2.
                                                                                                                       Sequence 97 AA;
                          Homo sapiens.
                                                   Shimkets RA,
 25-JUN-2002
                                 06-DEC-2001.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidaring cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBZ7737-ABBZ2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 16920; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 4; Length 98; 50.0%; Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wheat aspartyl-tRNA synthetase from clone wleln.pk0021.e6.
                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 16920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.6e
4; Mismatches
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                                                                   ABB63376 standard; protein; 98 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231.
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2000US-00614150.
                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL07479
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                                                                                                                                                                                                                                                                                                                                 pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interactions.
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11-JUL-2000;
                                                                                                                                                                                       26-MAR-2002
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                                                                                                                             ABB63376;
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         RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE03588
                                       ABB6337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1) in the specification). ABN15762 to ABN27525 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polymoucleotide syndrome associated with ORFX-associated disorder. ORFX polymoucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, of psoriasis, bening tumnours, keloid, degenerative disorders, haemornhage, of treatment of cancer, hyperproliferative disorders related to organ transplantation, cardiovascular diseases, disorders mallitus, systemic control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
                                                                                                                                         hyperproliferative disorder; psoriasis; benign tumour; haemorrhage, degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; ollesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did no form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pot sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                       frame; ORFX; gene therapy; cancer; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
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                                                          Human ORFX protein sequence SEQ ID NO:3154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-2001; 2001WO-US010836.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
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IEFISEDE 60
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9905-013622P

9905-013724P

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9905-0139453P

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99US-013946DP.
99US-013946ZP.
99US-013946ZP.
99US-0139763P.
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99US-0140695P.
99US-0140821P.
99US-0140991P.
99US-0141842P.
99US-0142154P.
99US-0128234P.
99US-0128714P.
99US-012945P.
99US-0130449P.
99US-0130510P.
99US-0130810P.
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990S-0132484P.
990S-0132485P.
990S-0132486P.
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99US-0142803P.
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99US-0143542P.
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99US-0144005P.
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99US-0144325P.
99US-0144331P.
                            16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
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-JUN-1999;
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18-JUN-1999;
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06-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is wheat aspartyl-tRNA synthetase of the invention. The aspartyl-tRNA synthetase are used as targets to facilitate designing and identification of inhibitors of the enzymes which are useful as herbicides. All or a substantial portion of the nucleic acid fragments of the present invention are used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information is useful in plant breeding in order to develop lines with desired phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                      New isolated polynucleotide encoding an aspartyl-tRNA synthetase useful as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 25; DB 4; Length 98; Pred. No. 1.6e+03; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 41798.
                                                                                                                                                                                                           Famodu LO, Orozco EM, Rafalski JA;
                                                                                                                                                                                                                                                                                                                                                     Claim 12; Col 33-36; 40pp; English.
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                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO (PION-) PIONEER HI-BRED INT INC.
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50.0%; P
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99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126784P.
99US-0126785P.
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CEFIGLDA 81
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Best Local Similarity
Matches 4; Conserv
   Triticum aestivum.
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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99US-0144632P
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99US-0145218P.
99US-0145224P.
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99US-0156596P.
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20-JUL-1999;
21-JUL-1999;
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22-JUL-1999;
22-JUL-1999;
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27-JUL-1999;
27-JUL-1999;
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10-SEP-1999;
13-SEP-1999;
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12-OCT-1999;
13-OCT-1999;
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28-JUL-1999;
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25-AUG-1999;
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17-AUG-1999)
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01-SEP-1999
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20-AUG-1999
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New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 25; DB 3; Length 99
Pred. No. 1.6e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acinetobacter baumannii protein #3608.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA36447 standard; protein; 99
                990S-0159295P
990S-0159331P
990S-01596331P
990S-0159633P
990S-0169633P
990S-0160741P
990S-0160770P
990S-0160770P
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990S-0160981P
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990S-016193P
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990S-0161350P
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QEFIVDDL 53
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N-PSDB; ADA32321.
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Best Local Similarity
Matches 4; Conserv
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                   13-0CT-1999

14-0CT-1999

14-0CT-1999

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14-0CT-1999

18-0CT-1999

21-0CT-1999

21-0CT-1999

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26-0C
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ADA36447

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Example; SEQ ID NO 7734; 328pp; English.

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       The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for baumannii protein.
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                              LSD1-interacting protein OO; plant pathogen response; apoptosis; programmed cell death; disease resistance; herbicide resistance; transgenic plant; crop protection.
                                                                                                                                                                   0
                                                                                                                                              Length 99;
                                                                                                                                            Score 25; DB 6; Length 99
Pred. No. 1.6e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       Pathogen response protein LSD1-interacting protein 00.
                                                                                                                                                                                                                                                                     AAW72393 standard; protein; 101 AA.
                                                                                                                                              100.08;
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                                                                                                                                                      50.0%;
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                                                                                                                                             Query Match 100.
Best Local Similarity 50.C
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
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                                                                                                                                                                                         1 XEFIXXDX 8
                                                                                                                        Sequence 99 AA;
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Arabidopsis thaliana. LSD1 interacting genes (see AAV66755-67) were isolated from a yeast gene expression library constructed in plasmid pJG4 solated from Arabidopsis leaves infected with Pseudomonas syringae. A two-hybrid system was used with LSD1 short and long open reading frames (see AAV66750-51) as bait. LSD1 (see AAW7236-67) is a novel polypeptide that regulates the initial response of plants to pathogens and the subsequent spread of plant cell death engendered by infection. Since the inactivation of LSD1 by mutation leads to enhanced disease resistance, enhanced resistance to pathogens. Thus, the invention includes all proteins (see AAW72384-96) that interact with the cell death regulator This is the amino acid sequence of LSD1-interacting protein 00 of Claim 46; Page 65; 88pp; English.

New isolated Arabidopsis genes - useful for producing transgenic plants which show resistance to cell death caused by pathogens or herbicides.

Epple PM;

Dietrich RA, Richberg MH,

Dangl JL,

WPI; 1998-531501/45.

N-PSDB; AAV66764

Sequence 101 AA;

·, designated ORF (open reading frame) 1-4534, and sequences ABN75054ABN79587 represent cDNAs encoding them. The invention also encompasses
polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
referred to as ORFX) proteins, polynucleotides at least 85% identical to
the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
polynucleotides, the recombinant production of ORFX proteins, antibodies
specific for ORFX proteins, methods of detecting ORFX polynucleotides and
activity, and methods of screening for modulators of ORFX expression or
activity, and methods of screening individuals for a predisposition to an
ORFX-associated disorder. The ORFX proteins of the invention have a wide
range of biological activities, such as cytokine, cell proliferation,
tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
chemokinetic activity, haemostatic activity, thrombolytic activity, Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antietherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide. Gaps Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ Sequences ABP31028-ABP35561 represent 4534 novel human proteins 0 Length 101; ; Score 25; DB 2; Length 10 Pred. No. 1.6e+03; 4; Mismatches 0; Indels Human ORF1675 protein, SEQ ID NO:3350. Claim 10; Page 1096; 2508pp; English. ABP32702 standard; protein; 103 AA. 100.08; 24-MAY-2001; 2001WO-US017076. 24-MAY-2000; 2000US-0206690P. 50.08; (first entry) 4; Conservative Leach MD, Shimkets RA; (CURA-) CURAGEN CORP. IEFICLDL 82 WPI; 2002-106200/14. æ Query Match Best Local Similarity Matches 4; Conserv 1 XEFIXXDX N-PSDB; ABN76728. transplantation WO200190366-A2 Homo sapiens. 08-JUL-2002 29-NOV-2001. ABP32702; ð 셤

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cc receptor/ligand, antinflammatory activity, tumour inhibition activity, and antinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. OFEX proteins, concluded antibodies may be used in the treatment of cancers, concluded actions and antibodies may be used in the treatment of cancers, concluded antibodies may be used in the treatment of cancers, contexpolated disorders such as psoriasis and benign tumours, contexpolated disorders such as epilepsy and Alaheimer's disease, cardiovascular diseases, immune system disorders; disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage diseases, and infectious diseases caused by viral, bacterial, chungal and other pathogens. ORRY mucleic acids may also be used as a source of primers and probes, in the detection of ORPX genomic sequences or transcripts, in the identification and cloning of homologous contensorables, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the configuration of ORFX-associated diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sato H, Ishii S;
C, Irie R, Tamec
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Pred. No. 1.7e+03;
Mismatches 0; Indels
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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4; Mismatches
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50.0%; F
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24-JAN-2002; 2002US-0350435P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein, SEQ ID 2020.
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Yoshikawa T,
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29 GEFIEGDK 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 103 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isogai T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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The present invention relates to novel human secretory or membrane

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                                                                                                                                                                                                                                                                                                                                  Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                                 Gaps
proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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0
                                                                                         Length 105;
                                                                                       Score 25; DB 6; Length 10
Pred. No. 1.7e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        Human nervous system related polypeptide SEQ ID NO 6027.
                                                                                                                                                                                                                              ABB17370 standard; protein; 106 AA.
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2000US-0180628P.
2000US-018464P.
2000US-0186350P.
2000US-0189874P.
2000US-0190176P.
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2000US-0214886P.
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2000US-0216647P.
2000US-0216880P.
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2000US-0217496P.
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2000US-0225759P.
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                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                 4; Conservative
                                                                                                                                                                 4 EEFIFYDY 11
                                                                                                                                         1 XEFIXXDX 8
                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                Sequence 105 AA;
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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07-JUL-2000;
07-JUL-2000;
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26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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28-JUN-2000;
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11-JUL-2000;
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14-AUG-2000;
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ABB17370
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29-SEP-2000; 2000US-023-3237P.
29-SEP-2000; 2000US-023-3237P.
29-SEP-2000; 2000US-023-3237P.
29-SEP-2000; 2000US-023-637P.
29-SEP-2000; 2000US-023-637P.
29-CCT-2000; 2000US-023-7039P.
02-OCT-2000; 2000US-023-7039P.
02-OCT-2000; 2000US-023-7039P.
02-OCT-2000; 2000US-023-7039P.
03-OCT-2000; 2000US-023-7039P.
03-OCT-2000; 2000US-023-703P.
03-OCT-2000; 2000US-023-703P.
03-OCT-2000; 2000US-023-703P.
03-OCT-2000; 2000US-023-703P.
03-OCT-2000; 2000US-023-703P.
03-OCT-2000; 2000US-024-178FP.
03-OCT-2000; 2000US-024-178FP.
04-NOV-2000; 2000US-024-1809P.
05-OCT-2000; 2000US-024-1809P.
06-NOV-2000; 2000US-024-17P.
08-NOV-2000; 2000US-024-64-7P.
08-NOV-2000; 2000US-024-64-7P.
08-NOV-2000; 2000US-024-64-7P.
08-NOV-2000; 2000US-024-65-23P.
22-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-02216868P.
23-AUG-2000; 2000US-02216868P.
23-AUG-2000; 2000US-022294P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
05-SEP-2000; 2000US-0229344P.
06-SEP-2000; 2000US-0229343P.
06-SEP-2000; 2000US-0229343P.
06-SEP-2000; 2000US-0229343P.
06-SEP-2000; 2000US-0229513P.
06-SEP-2000; 2000US-02295144P.
08-SEP-2000; 2000US-0229514P.
08-SEP-2000; 2000US-023144P.
08-SEP-2000; 2000US-023144P.
08-SEP-2000; 2000US-023196P.
14-SEP-2000; 2000US-023290P.
14-SEP-2000; 2000US-023299P.
14-SEP-2000; 2000US-0233064P.
14-SEP-2000; 2000US-0233064P.
12-SEP-2000; 2000US-0233063P.
27-SEP-2000; 2000US-02333063P.
27-SEP-2000; 2000US-0233336P.
27-SEP-2000; 2000US-02333336P.
27-SEP-2000; 2000US-0233336P.
27-SEP-2000; 2000US-02333336P.
27-SEP-2000; 2000US-0233336P.
27-SEP-2000; 2000US-02333336P.
27-SEP-2000; 2000US-0233336P.
27-SEP-2000; 2000US-0233336P.
27-SEP-2000; 20
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB146'08-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. In the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, or solated as set of solated and other cancer. Inver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, cardiovascular disorders such as myocardial ischaemias; (d) wound healing (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) cardiovascular diseases such as viral, bacterial, fungal and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly come with the printed specification, but was obtained in electronic format directly come in the printed specification.
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2000US-0249207P

2000US-0249209P

2000US-0249211P

2000US-0249212P

2000US-0249213P

2000US-0249213P

2000US-0249213P

2000US-0249213P

2000US-0249214P

2000US-0249214P

2000US-0249216P

2000US-0249216P

2000US-0249244P

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N-PSDB; ABA13696.
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Gaps

·: 0

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Local Similarity

Best Loc Matches

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21

1 XEFIXXDX 8

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us-09-660-302e-1.rag

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The invention relates to isolated nucleic acids encoding plant stress response proteins (including peptide-methionine sulphoxide reductases) appearing as ABMUS8148 46 (or a protein 80% identical to them) from a pertaing as ABMUS8148 46 (or a protein 80% identical to them) from a mays, Oryza sativa, Glycine max, or Triticum aestivum. Also included are expression cassettes, transformed host cells, transgenic plants/seeds, modulating the level of peptide-methionine sulphoxide reductase in a plant and a computer system/data processing system for identifying, analysing, or modelling a genetic sequence. The plant nucleic acid is useful in developing strategies to improve plant response to stress (e.g. drought, heat, radiation or pathogen attack), engineering plants with increased disease and stress resistance, manipulating DNA repair and recombination efficiency, manipulating intracellular protein transport, and improving/protecting grain flavour. The nucleic acids may also be used as probes or amplification primers in the detection, quantitation or isolation of gene transcripts, for recombinant expression of encoded polypeptides, as immunogens in preparing or screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptide-methionine sulfoxide reductase and nucleic acids, useful in improving plant response to stress, engineering plants with increased disease and stress resistance, or and improving/protecting grain flavor.
                                                                                                                                                                                                                                           Plant; EST; expressed sequence tag; stress response; drought; heat; radiation; pathogen attack; grain flavour; disease resistance; peptide-methionine sulphoxide reductase; DNA repair; enzyme; intracellular protein transport.
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                      ABU58228 standard; protein; 106 AA.
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                                                                                                                                                                                        Wheat stress response protein #18.
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Weng Z;
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99US-0133427P.
99US-0133428P.
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99US-0137667P.
2000US-00566394.
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                                                                                                                                  (first entry)
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PRAMODU O O.
MEYERS B C.
MIAO G.
ODELL J T.
RAFALSKI J A.
THORPE C J.
SAKAI H.
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Sakai H,
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N-PSDB; ABX78399.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-2002;
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                                                                                                                                  14-APR-2003
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11-MAY-1999;
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(THOR/)
(SAKA/)
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(MEYE/)
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ABU58228
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antibodies, and in sense or antisense suppression of one or more genes in a host cell, tissue or plant. The proteins may be used as immunogens or antigens to obtain antibodies specifically immunoreactive with the protein, and in assays for enzyme agonists or antagonists. The present sequence is a plant stress response protein (or fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             equivalent of sequences hybridising to [1]. Also included are a recomplement or sequences hybridising to [1]. Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection, and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans and vaccines containing the nucleic acid are useful for recombinant production of candida albicans and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents one if the disclosed E. faecium proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid derived from blaterococcus faecium encoding an Entercoccus faecium enclypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid derived from Enterococcus faecium encoding an
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                                                                                                                                                               Length 106;
                                                                                                                                                           ; Score 25; DB 6; Length 10
Pred. No. 1.7e+03;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E. faecium protein sequence SEQ ID 7131.
                                                                                                                                                                                                                                                                                                                                                                              ADC97504 standard; protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                             100.0%;
50.0%; I
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98US-0085598P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00107532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecium.
                                                                                                                                                                                                                                                                 :|||::|:
71 SEFIKTDA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2003-799836/75.
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                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADC93850
                                                                                                                          Sequence 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6583275-B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                      ADC97504;
                                                                                                                                                                                                                                                                                                                                             80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that are highly expressed in uterine mourtissue and which have anticancer and cytostatic activity. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling BSTs (expressed expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. ANY59941-Y60328 represent protein fragments encoded by the human endometrium tumour cDNA library derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid sequences expressed in uterine cancer tissues, and derived polypeptides, for treatment of uterine and endometrial cancer and identification of therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dahl E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel human nucleic acid (cDNA) sequences (A)
                                                                            Gaps
                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hinzmann B, Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                  вычометгічт, пчтат, tumour; cancer; anticancer; cytostatic;
EST: treatment; uterine; gene therapy; expressed sequence tag.
                                            Length 106;
                                         Score 25; DB 7; Length 10
Pred. No. 1.7e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    Human endometrium tumour EST encoded protein 98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST fragments represented in AAZ41981-Z42121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                     AAY60038 standard; protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 23; Page 314; 444pp; German.
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                                         100.0%;
50.0%; I
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                                                                            Conservative
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Best Local Similarity
4, Conserve
                        Query Match
Best Local Similarity
4; Conserve
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75 MEFIKEDY 82
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                                                                                                          1 XEFIXXDX 8
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             Sequence 106 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
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                                                                                                                                                                                                                                                       AAY60038;
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that are applied to plant crops to protect them from insect damage. The polymocleotides may be used in the production of transgenic plants that express the insecticidal polypeptides and consequently have improved insect resistance compared to non-transformed plants. Monocotyledonous or dicotyledonous plants may be protected in this way, for example corn, wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato, tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry, fruit, legume, vegetable, ornamental plant, shrub, cactus and/or treefort. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm, cotton leaf perforator and spruce budworm) may be affected by application of the insecticidal polypeptides (full details given in specification)
                                                                                                                                                                                                                                                  transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum; sugarcane; tomaco; tobacco; kapok; flax; potato; barley; turf grass; pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub; cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm; cotton leaf perforator; CryET44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides and the polynucleotides that encode them, useful for increasing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents a B. thuringiensis Lepidopteran-active delta-endotoxin, crystal protein CryET44. The Lepidopteran-active B. thuringiensis delta-endotoxin polypeptides may be used as compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                   Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·
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Pred. No. 1.8e+03;
4; Mismatches 0; Indels
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                                                                                                                                                                                                B. thuringiensis toxic crystal protein, CryET44.
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                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG10474 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 108; 173pp; English.
                                                                                        AAU02024 standard; protein; 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insect resistance of plant.
                                                                                                                                                            29-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                Bacillus thuringiensis.
QEFIDSDA 67
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les 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  40200119859-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-2001
                                                                                                                          AAU02024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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ID AAG1
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Gaps

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100.0%; Score 25; DB 2; Length 108; 50.0%; Pred. No. 1.7e+03; 1ive 4; Mismatches 0; Indels

Conservative

1 XEFIXXDX 8

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9904S-0139463P-9904S-0139750P-9904S-0139750P-9904S-0139750P-9904S-0139817P-9904S-0140854P-9904S-0140854P-9904S-0140854P-9904S-0140894P-9904S-0140894P-9904S-0140894P-9904S-014292P-9904S-0142332P-9904S-014292P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145348P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145244P-9904S-0145348P-9904S-0145348P-9904S-0145348P-9904S-0145348P-9904S-0145348P-9904S-0145348P-9904S-0145348P-9904S-0145348P-9904S-0145348P-9904S-0145348P-9904S-0145348P-9904S-0145348P-9904S-0149348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-0149948P-9904S-014994348P-9904S-014994348P-9904S-014994348P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-01499448P-9904S-0149
18-JUN-1999

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10-JUL-1999

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27-JUL-1999,
28-JUL-1999,
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05-AUG-19
05-AUG-19
06-AUG-19
  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 8813
                                                                                                                                                                                                                                     99US - 01231800

99US - 012548P

99US - 012678P

99US - 012678P

99US - 012678P

99US - 0128714P

99US - 0128714P

99US - 013844P

99US - 0130449P

99US - 0130449P

99US - 0131449P

99US - 0131449P

99US - 0131448P

99US - 013248PP

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990S-0138094P.
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990S-0139119P.
990S-0139452P.
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990S-0139456P.
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990S-0139456P.
                                                                                                                                                                                                   2000EP-00301439
                          (first entry)
                                                                                                                          Arabidopsis thaliana
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25-MAR-1999,
01-APR-1999,
01-APR-1999,
06-APR-1999,
16-APR-1999,
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19-APR-1999,
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06-MAY-1999,
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25-MAY-1999;
27-MAY-1999;
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                          17-0CT-2000
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 AAG10474;
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14-MAY-1
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hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                          990S-0121825P

990S-0123180P

990S-0125788P

990S-0126264P

990S-0126284P

990S-0127462P

990S-0128234P

990S-0130891P

990S-0130891P

990S-0130891P

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990S-0130891P

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                                                                           2000EP-00301439
                         Arabidopsis thaliana
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09-MAR-1999;
23-MAR-1999;
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30-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                          EP1033405-A2
                                                                                                                                                                                                                                                                                                                                  -MAY-1999;
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- JUN-1999;
- JUN-1999;
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08-JUN-1999
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05-MAY-1999
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                                                           06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 110;
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Pred. No. 1.8e+03;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG24527 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                           9905-0155596P

9905-0157117P

9905-0157538-

9905-0158029P

9905-0158029P

9905-0158238-

9905-0159294P

9905-0159294P

9905-0159294P

9905-0159319P

9905-0159311P

9905-0159634P

9905-0159634P

9905-0159634P
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990S-0160980P.
990S-0160981P.
990S-0160989P.
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99US-016136DP.
99US-016136DP.
99US-016192DP.
99US-0161932P.
99US-0161932P.
 99US-0150884P.
99US-0151065P.
99US-0151060P.
99US-0151080P.
99US-0151303P.
99US-0151310P.
99US-015373P.
99US-015373P.
99US-015373P.
99US-015403P.
99US-015403P.
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99US-0160770P.
99US-0160814P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
ilarity 50.0%;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                   99US-0161405P
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4; Conserva
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IEFICLDL
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22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
10-SEP-1999;
110-SEP-1999;
12-SEP-1999;
12-SEP-1999;
23-SEP-1999;
24-SEP-1999;
24-SEP-1999;
25-SEP-1999;
26-OCT-1999;
13-OCT-1999;
13-OCT-1999;
14-OCT-1999;
12-OCT-1999;
13-OCT-1999;
14-OCT-1999;
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21-OCT-1999;
21-OCT-1999;
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22-0CT-1999
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Best Local S:
Matches 4
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99US-0140823P.
99US-0140991P.
99US-0141842P.
99US-0142154P.
99US-014230P.
99US-014230P.
99US-014230P.
99US-0143542P.
99US-014364P.
99US-0144086P.
99US-0144086P.
99US-014433P.
99US-0144332P.
99US-0144333P.
99US-0144333P.
                                                                                                                                                                                                                    990S-0144814P

990S-0145086P

990S-0145089P

990S-0145089P

990S-0145089P

990S-0145192P

990S-0145218P

990S-0145218P

990S-0145218P

990S-0145218P

990S-0145218P

990S-0145318P

990S-0145318P

990S-0145386P

990S-0145386P

990S-0145386P

990S-0147204P

990S-0147204P

990S-014720P

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990S-0148684P

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990S-0148684P

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990S-0148620P

990S-0149920P

990S-0149920P

990S-0149920P

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990S-0149920P
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99US-0151065P.
99US-0151080P.
99US-0151303P.
99US-0151438P.
99US-0151438P.
 99US-0140695P
24 - JUN - 1999;
28 - JUN - 1999;
30 - JUN - 1999;
01 - JUL - 1999;
02 - JUL - 1999;
04 - JUL - 1999;
06 - JUL - 1999;
06 - JUL - 1999;
12 - JUL - 1999;
13 - JUL - 1999;
14 - JUL - 1999;
16 - JUL - 1999;
16 - JUL - 1999;
16 - JUL - 1999;
17 - JUL - 1999;
18 - JUL - 1999;
19 - JUL - 1999;
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21-JUL-1999;
21-JUL-1999;
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03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
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22-JUL-1999;
22-JUL-1999;
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13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
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25-AUG-1999;
26-AUG-1999;
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20-JUL-1999;
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09-AUG-1999;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB 3; Length 11
Pred. No. 1.8e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MLHR comparison related HU.IGEREC amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR57093 standard; peptide; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
         990S-0153070P.
990S-015403P.
990S-015403P.
990S-015473P.
990S-0155486P.
990S-015565P.
990S-015565P.
990S-015658P.
990S-015658P.
990S-015658P.
990S-015753P.
990S-015753P.
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990S-0159330P
990S-0159331P
990S-0159637P
990S-0159634P
990S-0160741P
990S-0160741P
990S-016070P
990S-0160981P
990S-0160981P
990S-0160981P
990S-0160981P
990S-0160981P
990S-0161981P
990S-0161981P
990S-0161981P
990S-0161981P
990S-0161361P
990S-0161361P
990S-0161361P
990S-0161361P
                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
ilarity 50.0%;
Conservative 4
 99US-0152363P
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 4; Conserv
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84 IEFICLDL
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10-SEP-1999;

10-SEP-1999;

15-SEP-1999;

16-SEP-1999;

20-SEP-1999;

22-SEP-1999;

22-SEP-1999;

24-SEP-1999;

24-SEP-1999;

26-OCT-1999;

06-OCT-1999;

07-OCT-1999;

13-OCT-1999;

14-OCT-1999;

14-OCT-1999;

14-OCT-1999;

14-OCT-1999;

14-OCT-1999;

14-OCT-1999;

18-OCT-1999;

18-OCT-1999;

18-OCT-1999;

18-OCT-1999;

18-OCT-1999;

18-OCT-1999;

18-OCT-1999;

18-OCT-1999;

18-OCT-1999;

18-OCT-1999;
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25-OCT-1999;
25-OCT-1999;
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21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
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26-OCT-1999;
26-OCT-1999;
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28-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                      21-OCT-1999;
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Best Local S
Matches 4
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ABR57093
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Rupar MJ;

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The sequence represents a B. thuringiensis Lepidopteran-active deltaendotoxin, crystal protein CryET45. The Lepidopteran-active B. thuringiensis delta-endotoxin polypeptides may be used as compositions that are applied to plant crops to protect them from insect damage. The polymuclectides may be used in the production of transgenic plants that express the insecticidal polypeptides and consequently have improved insect resistance compared to non-transformed plants. Monocotyledonous or dicotyledonous plants may be protected in this way, for example corn, wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato, tobacco, kapok, flax, potato, barley, tuff grass, pasture grass, berry, totacco, kapok, flax, potato, barley, tuff grass, pasture grass, berry, totacco, kapok, flax, potato, barley, tuff grass, pasture grass, berry, totacco, kapok, day, presented plant, shrub, cactus and/or tree cell. A wide range of insects (e.g gypsy moth, looper, tobacco budworm, cotton leaf perforator and spruce budworm) may be affected by application of the insecticidal polypeptides (full details given in specification)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                        Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides and the polynucleotides that encode them, useful for increasing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 25; DB 4; Length 113;
Pred. No. 1.8e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 42237.
                                                                                                                                                 Gilmer AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG34679 standard; protein; 114 AA.
                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 109; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-0126785P.
99US-012648P.
                                                                                                                                                 Donovan WP,
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13-SEP-2000; 2000WO-US025361.
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                                                 99US-0153995P
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                                                                                                                                                                                                                                                                                                                            insect resistance of plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-2000 (first entry)
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                                                                                                                                                                                                  2001-281518/29.
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87 VEFIPVDA 94
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                                                                                                  (MONS ) MONSANTO CO
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                                                                                                                                                   chu c,
                                                                                                                                                                                                  WPI; 2001-281518,
N-PSDB; AAS02468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 113 AA;
                                                 15-SEP-1999;
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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                                                                                                                                                   Baum JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a polypeptide (I) containing an the memoglobulin (Ig) heavy chain dimer having no Ig light chain in which the amino acid sequence of a ligand-combined partner is a receptor, a carrier protein, a hormone, a growth factor, an ersceptor, a carrier protein, a hormone, a growth factor, an expensive or a nutritive or substance, but is not a subunit polypeptide encoded by a lymphocyte inducing receptor, an Ig gene super family-constituting element, a protein homologous to it, or a separated gene substitute of the variable region of at least one Ig heavy chain. Its combined partner is fused with the amino acid sequence of an Ig stationary region at its C-end and maintains its combining feature. Also described: (I) a nucleic acid cacid of (I); (2) a replicable expression vector containing the nucleic acid of (I); (3) a composition containing cells transformed by the expression vector of (2); and (4) producing (I), comprising culturing the cypression vector of (2); and (4) producing (I), comprising culturing the cyplypeptide is recovered from the cells are cultured and the polypeptide is recovered from molecule and a ligand. In an example from the containing the resent invention mouse lymphocyte cell surface glycoprotein designated LHR (MLHR) was isolated from a mouse spleen and alload. The present sequence represents an amino acid sequence given in comparison with an MLHR amino acid sequence, which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delta endotoxin, Lepidopteran-active, crystal protein, insecticide, transgenic plant; corn, wheat; soybean; oat; cotton; rice; rye; sorghum; sugarcane; tomato; tobaco; kapok; flax; potato; barley; turf grass; pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub; cactus; tree cell; gypsy moth, looper; tobacco budworm; spruce budworm; cotton leaf perforator; CryET45.
                                                                                                                                                                                                                                                                        A fused protein consisting of a ligand-combined protein and a stable plasma protein, a polypeptide, a nucleic acid, a replicable expression vector, a composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU02025 standard; protein; 113 AA
                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 11; 44pp; Japanese.
                                                                                                89US-00444625
91JP-00501520
                                                 21-NOV-1990; 2002JP-00026825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus thuringiensis
                                                                                                                                                                        (GETH ) GENENTECH INC.
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GEFIWVDG 65
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                                                                                                                                                                                                                       WPI; 2003-407283/39
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 110 AA;
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                                                                                                22-NOV-1989;
21-NOV-1990;
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Gaps

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22-OCT-1999

26-OCT-1999 26-OCT-1999 28-OCT-1999 28-OCT-1999 28-OCT-1999 29-OCT-1999

22-OCT-1999

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acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or blodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent operent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at the production of 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents a B. thuringiensis Lepidopteran-active delta-endocoxin, crystal protein CryET56. The Lepidopteran-active B. thuringiensis delta-endocoxin polypeptides may be used as compositions that are applied to plant crops to protect them from insect damage. The polynucleotides may be used in the production of transgenic plants that express the insecticidal polypeptides and consequently have improved insect resistance compared to non-transformed plants. Monocotyledonous or dicocyledonous plants may be protected in this way, for example corn, wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato, tobacco, xapok, flax, poatto, barley, turf grass, pasture grass, berry, fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delta endotoxin; Lepidopteran-active; crystal protein; insecticide; transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum; sugarcane; tomarc; tobacco; kapok; flax; potato; barley; turf grass; pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub; cactus; tree cell; gypsy moth, looper; tobacco budworm; spruce budworm; cotton leaf perforator; CryET56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides and the polynucleotides that encode them, useful for increasing the
                                                                                                                                                                                                                           Score 25; DB 5; Length 114;
Pred. No. 1.8e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rupar MJ;
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                                                                                                                                                                                                                                                                     4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02032 standard; protein; 116 AA.
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                                                                                                                                                                                                                             100.0%;
50.0%; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis.
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Best Local Similarity
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22 GEFIVCDE
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                                                                                                                                                                                            Sequence 114 AA;
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                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleotide sequence useful in the identification or Lactococcus lactis and related species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 25; DB 3; L
Pred. No. 1.8e+03;
4; Mismatches 0;
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                                     990S-0159330P.
990S-0159331P.
990S-0159637P.
990S-0159638P.
                                                                                                                                 99US-0160741P.
99US-0160767P.
99US-0160768P.
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99US-0161406P.
99US-0161359P.
99US-0161360P.
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99US-0161993P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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IEFICLDL 112
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                                     14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
                                                                                                                                                                                      21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
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25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
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16-MAY-2002
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Query Match Matches 105

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RESULT 88 ABB54747 ABB54747;

Bolotine A,

12-OCT-2001

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid moding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding cantisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway confideration, (7) identifying a compound that inhibits cellular proliferation, (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound; a activity; (11) a culture comprising strains in which the gene compound a activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in which the gene
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cotton leaf perforator and spruce budworm) may be affected by application of the insecticidal polypeptides (full details given in specification)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW;
Xu HH;
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                      ;
                                                                                               Score 25; DB 4; Length 116; Pred. No. 1.9e+03;
                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #676.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 43073; 1766pp; English.
                                                                                                                  Pred. No. 1.9e
4; Mismatches
                                                                                                                                                                                                                                                                                                                 ABU15149 standard; protein; 116 AA.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
                                                                                           100.0%;
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                                                                                                                                      4; Conservative
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FEFIPVDA 102
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Trawick JD,
                                                                                                                                                                           1 XEFIXXDX 8
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                                                                                             Query Match
Best Local Similarity
Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
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                                                         Sequence 116 AA;
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08-FEB-2002;
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Wall D,
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to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this pattent din not form part of the printed specification, but was obtained fire.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leinamycin biosynthesis gene cluster; Lmn; open reading frame; ORF; anti-tumour antibiotic; broad spectrum antimicrobial activity; Gram-positive; Gram-negative bacteria; chemical modification; metabolite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of the Streptomyces atroolivaceus leinamycin (Lnm) blosynthesis gene cluster containing 71 open reading frames (ORFs ) (ORFs -35 through -1, ORFs lnm& through lnm², and ORFs +1 through +9). Leinamycin is a novel anti-tumour antibiotic produced by several Streptomyces species. It exhibits broad spectrum antimicrobial activity against Gram-positive and Gram-negative bacteria, but not against fungi. The polypeptides encoded by the Lnm biosynthesis gene cluster ORFs are useful for chemically medifying a molecule in a host cell. The host cell is a bacterium or eukaryotic cell, including a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    apo-carrier protein; holo-carrier protein; tumour; polyketide;
hybrid polypeptide/polyketide metabolite; Lnm production; cytostatic.
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by S. atroolivaceus leinamycin gene cluster ORF 1nmV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel gene cluster responsible for synthesis of leinamycin in
Streptomyces atroolivaceus useful for making various peptide and/or
polyketide, and/or hybrid polypeptide/polyketide metabolites.
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                                                                                                                                                                                                                                                                                                                Score 25; DB 6; Length 116; Pred. No. 1.9e+03; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     50.0%, Pred. No. 1.96
ive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU11397 standard; protein; 120 AA.
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                                                                                                                                                                                                                                                                                                                100.08;
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                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                            Sequence 116 AA;
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Matches
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99US-0145192P.
99US-0145145P.
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            cc mammalian, yeast, plant, fungal, or insect cell. The molecule is an endogenous metabolite produced by the host cell or exogenously supplied metabolite, or an anino acid, and the polypeptide is a peptide synthetase cor amino transferase. The polypeptides encoded by the Imm gene cluster are useful for converting an apo-carrier protein to a holo-carrier protein. Inm shows potent antitumour activity in tumour models in vivo. The Inm gene cluster modules and/or catalytic domains are useful for making various peptide and/or polyketide, and/or hybrid polypeptide/polyketide metabolites. The proteins encoded by the ORFs are useful alone, or in combination with other active domains to modify various target substrates. The Imm gene cluster is useful to upregulate endogenous Imm production to permit Imm production in cells and/or to make various modified Imm. Inm, its analoque, or other polyketide, competide or hybrid polyketide/peptide metabolites are useful as the peptide or hybrid polyketide/peptide metabolites are useful as the proteins encoded by or offer of metabolites. ABUI1311-ABUI1411 represent the proteins encoded by or offer offer of the S. atroolivaceus leinamycin blosynthesis gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 1.9e+03;
4; Mismatches 0; Indels
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50.0%; F
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99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-0126785P.
99US-0126785P.
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99US-0129845P.
99US-0130077P.
99US-013049P.
99US-0130891P.
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99US-0132486P.
99US-0132487P.
99US-0132863P.
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99US-0132484P
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Best Local Similarity 50.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 120 AA;
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05-MAR-1999,
09-MAR-1999,
23-MAR-1999,
25-MAR-1999,
01-APR-1999,
06-APR-1999,
16-APR-1999,
119-APR-1999,
21-APR-1999,
21-APR-1999,
21-APR-1999,
23-APR-1999,
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06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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30-APR-1999
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04-MAY-1999
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99US-0159330P.
99US-0159331P.
99US-0159637P.
99US-0159638P.
               99US-0145224P.
99US-0145276P.
99US-0145913P.
99US-0145918P.
99US-0145919P.
99US-0145951P.
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99US-0158029P.
99US-0158232P.
99US-0158369P.
99US-0159293P.
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99US-0160767P.
99US-0160768P.
99US-0160770P.
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99US-0160815P.
99US-0160980P.
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99US-0157753P.
                                                  27 - JUL - 1999;
27 - JUL - 1999;
28 - JUL - 1999;
02 - ANG - 1999;
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27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
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11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
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16-AUG-1999;
17-AUG-1999;
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15-SEP-1999;
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23-AUG-1999;
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26-AUG-1999;
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24-SEP-1999;
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                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated canine low affinity immunoglobulin B receptor nucleic ac
molecule, useful for protecting canids from diseases mediated by the
receptor, such as allergy, atopic dermatitis, asthma, and hay fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Canine; immunoglobulin E; IgE; CD23; antiallergic; antiasthmatic; antiinflammatory; dermatological; gene therapy; vaccine; receptor.
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                                                                                                                                                                           DB 3; Length 121;
                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                       2e+03;
                                                                                                                                                                          k; Score 25; DB
; Pred. No. 2e+03
4; Mismatches
                                                                                                                                                                                                                                                                                                                          ABB81063 standard; protein; 123 AA.
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99US-0160981P.
99US-0160989P.
99US-0161404P.
99US-0161406P.
99US-0161359P.
99US-0161361P.
99US-0161920P.
99US-0161932P.
99US-0161932P.
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50.0%; E
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                                                                                                                                                                                                     4; Conservative
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104 LEFIEEDE 111
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                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                          26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
                                                                 26-OCT-1999;
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Best Local Si
Matches 4,
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RESULT 94

AAG01456

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hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                           Protein identification; signal transduction pathway; metabolic pathway;
                Arabidopsis thaliana protein fragment SEQ ID NO: 42032
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9905-0123180P

9905-0126788P

9905-0126788P

9905-0126788P

9905-0126788P

9905-0126784P

9905-0128714P

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9905-0130419P

9905-0132448P

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9905-013248P

9905-0134218P

9905-0136782P

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9905-0137528P

9905-01388440P

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9905-01388440P
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99US-0139750P.
99US-0139763P.
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                                                                                                   Arabidopsis thaliana.
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08-APR-1999;
16-APR-1999;
                                                                                                                             EP1033405-A2
                                                                                                                                                                                                                                                                                 -MAR-1999;
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-MAY-1999;
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-JUN-1999;
-JUN-1999;
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11-MAY-1999;
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21-APR-19
23-APR-19
23-APR-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a polypeptide encoded by one of a large number of 5. ESTs derived from mRNAs encoding secreted proteins. The 5. ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3. untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5. ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the fill 5. UTR is rarely included. 5. ESTs are derived from mRNAs with intact 5. ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5. ESTs mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                            Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; SEQ ID NO 5537; 71pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Duclert A, Giordano J;
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4; Mismatches
                                                                                                                                                                                 Human secreted protein, SEQ ID NO: 5537.
                                                                                              AAG01456 standard; protein; 124 AA.
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                                                                                                                                                                                                                          gene therapy; chromosome mapping
                                                                                                                                                                                                                                                                                                                                      21-FEB-2000; 2000EP-00200610.
                                                                                                                                                                                                                                                                                                                                                                  99US-0122487P.
                                                                                                                                                    (first entry)
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113 EEFIFYDY 120
                :|||::|:
73 GEFIWMDE 80
1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC01462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                            (GEST ) GENSET
                                                                                                                                                                                                                                                    Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1999;
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                                                                                                                                                    06-OCT-2000
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                                                                                                                           AAG01456;
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18-JUN-1999

18-OCT-2000 (first entry)

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AAG34531

Matches

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99US-0139817P.
99US-0140899P.
99US-0140839P.
99US-0140839P.
99US-0140839P.
99US-0140839P.
99US-0141287P.
99US-0141287P.
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99US-01421842P.
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990S-0148565P.
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99US-0149723P.
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99US-0149902P.
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99US-0151065P.
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21 - JUN - 1999;
22 - JUN - 1999;
23 - JUN - 1999;
24 - JUN - 1999;
26 - JUN - 1999;
30 - JUN - 1999;
30 - JUN - 1999;
30 - JUL - 1999;
30 - JUL - 1999;
30 - JUL - 1999;
31 - JUL - 1999;
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19-UUL-1999;
19-UUL-1999;
20-UUL-1999;
20-UUL-1999;
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27-AUG-1999;
27-AUG-1999;
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23-JUL-1999;
23-JUL-1999;
26-JUL-1999;
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27-JUL-1999;
27-JUL-1999;
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20-AUG-1999;
20-AUG-1999;
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21-JUL-1999;
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Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nochropic; neuroprotective; antibacterial; virucide; fundicide; optialmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder;
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Pred. No. 2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human novel secreted protein, Seg ID 1512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU16559 standard; protein; 125 AA
990S-0151080P-
990S-0151333P-
990S-0151333P-
990S-015333P-
990S-0153758P-
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990S-01696P-
990S-01609P-
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QEFIVDDL 53
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Best Local Similarity
27-AUG-1999;
30-AUG-1999;
30-AUG-1999;
01-SEP-1999;
13-SEP-1999;
13-SEP-1999;
13-SEP-1999;
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24-SEP-1999;
25-SEP-1999;
25-SEP-1999;
26-SEP-1999;
27-SEP-1999;
28-SEP-1999;
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cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer; disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                 2000US-0184664P

2000US-0184664P

2000US-0184664P

2000US-0189874P

2000US-0190076P

2000US-029467P

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2000US-022644P

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2000US-022629P
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2000US-022109P
                                                                                                         2001WO-US001341
                                                                       WO200155322-A2
                                                       Homo sapiens
                                                                                                         17-JAN-2001;
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2000US-0233065P.
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2000US-024629P.
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21.58P-2000;
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New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
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2000US-0225447P.
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2000US-0240960P.
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                                                                  17-JAN-2001; 2001US-00764864
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N-PSDB; ABX73887.
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(BARA/) BARASH S C.
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14-AUG-2000;
22-AUG-2000;
30-AUG-2000;
01-SEP-2000;
                                                                                                                             04-FEB-2000;
28-70N-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
14-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-ANG-2000;
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05-SEP-2000;
05-SEP-2000;
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25-SEP-2000;
27-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
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02-OCT-2000;
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01-SEP-2000;
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21-SEP-2000;
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13-OCT-2000;
                      19-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated nucleic acid molecules and their can concoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a also used in diagnosing a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunossays e.g. radioimmunossays or enzyme linked immunosorbant assays (BLISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. carchiac arrest, carebrovascular disorders e.g. carchiac arrest, carebrovascular disorders e.g. cerebral ischaemia, anglogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithalial cell proliferation, to pervent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                             New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; neural disorder; immune system disorder; renal disorder;
muscultar disorder; respiratory disease; reproductive disorder;
gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
hyperproliferative disorder; inflammatory disease; allergic reaction;
blood related disorder; inflammatory disease; allergic reaction;
blood related disorder; cancer; immunosuppressive; antinflammatory;
cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
haemostatic; antiateriosclerotic.
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Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID NO 1512; 980pp; English
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                                                                                                                                                        Rosen CA, Barash SC, Ruben SM;
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50.0%; F
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08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0259679P.
05-JAN-2001; 2001US-0259678P.
                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
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25 AEFIKRDD 32
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990S-013533P

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990S-013532P

990S-0136392P

990S-0136782P

990S-0137528P

990S-0137728P

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990S-0139455P

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990S-0139763P.
990S-013989P.
990S-0140353P.
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990S-0141287P.
990S-0141287P.
990S-0142154P.
990S-0142330P.
990S-0142803P.
990S-0142803P.
990S-0144085P.
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99US-0139462P.
99US-0139463P.
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99US-0145224P
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              14 - MAY - 1999;
18 - MAY - 1999;
20 - MAY - 1999;
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24 - MAY - 1999;
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21-JUN-1999;
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        polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. system) clubus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. and multiple sclerosis), muscular disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and appendicitis), allergic reactions and conditions (e.g. asthma), blood appendicitis), allergic reactions and conditions (e.g. asthma) blood infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and ABUS5748 represent human novel polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway, hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                         Gaps
                                                                                                                                                                                          0
                                                                                                                                                                    100.0%; Score 25; DB 6; Length 125; 50.0%; Pred. No. 2e+03; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 3533.
                                                                                                                                                                                                                                                                            AAG06674 standard; protein; 126 AA.
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99US-0123180P.
99US-012548P.
99US-0125788P.
99US-01264P.
99US-0127462P.
99US-0128234P.
99US-0128234P.
99US-0130891P.
99US-0130891P.
99US-013081P.
99US-0132848P.
99US-0132484P.
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Best Local Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                             termination sequence.
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25 AEFIKRDD 32
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                                                                                                                                                  Sequence 125 AA;
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05-MAR-1999;
09-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
16-APR-1999;
11-APR-1999;
11-APR-1999;
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23.APR-1999;
28.APR-1999;
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4.MAY-1999;
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PR 27-UM-1999; 99US-0145913P.
PR 28 27-UM-1999; 99US-0145913P.
PR 28 20-UM-1999; 99US-0145913P.
PR 02-MUG-1999; 99US-0145913P.
PR 02-MUG-1999; 99US-0145318P.
PR 02-MUG-1999; 99US-0145318P.
PR 02-MUG-1999; 99US-0147302P.
PR 03-MUG-1999; 99US-0147302P.
PR 04-MUG-1999; 99US-0147302P.
PR 04-MUG-1999; 99US-0147302P.
PR 13-MUG-1999; 99US-0147302P.
PR 12-MUG-1999; 99US-0147302P.
PR 13-MUG-1999; 99US-0147302P.
PR 13-MUG-1999; 99US-014732P.
PR 13-MUG-1999; 99US-014732P.
PR 13-MUG-1999; 99US-014732P.
PR 13-MUG-1999; 99US-0149722P.
PR 13-MUG-1999; 99US-0149722P.
PR 13-MUG-1999; 99US-0149722P.
PR 27-MUG-1999; 99US-0154066P.
PR 27-MUG-1999; 99US-015406P.
PR 27-MUG-1999; 99US-015506P.
PR 27-MUG-1999; 99US-015506P.
PR 27-SEP-1999; 99US-015506P.
PR 27-SEP-
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                                                                                                                     Gaps
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                                                                                                  3; Length 126;
                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 42798
                                                                                                 100.0%; Score 25; DB 3; 50.0%; Pred. No. 2e+03; ive 4; Mismatches
                                                                                                                                                                                                           AAG35079 standard; protein; 126 AA
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990S-0123180P

990S-012548B

990S-0126264P

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990S-01262845P

990S-0128234P

990S-0128234P

990S-0130077P

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990S-0130077P

990S-0130891P

990S-0132448P

990S-0132484P

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99US-013421P.
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99US-0134941P.
99US-01354P.
99US-013553P.
990S-0161406P.
990S-0161359P.
990S-0161359P.
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                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
11-MAY-1999;
21-MAY-1999;
21-MAY-1999;
 25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
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Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                 100.0%; Score 25; DB 3; Length 126; 50.0%; Pred. No. 2e+03;
                                                                        Pred. No. 2e+(
                                                                                                                                                                                                 Novel human diagnostic protein #3461.
                                                                                                                                                    ABG03470 standard; protein; 126 AA.
Mon Sep 13 10:53:31 2004
                                                                        ilarity 50.0%; Pr
Conservative 4;
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                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-00540217.
                                                                                                                                                                                                                                                                                                           23-AUG-2000; 2000US-00649167.
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                                         99US-0161993P.
99US-0162142P.
                                                                                                                                                                                  (first entry)
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46 QEFIVDDL 53
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                                                               Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS67657.
                                                                                                                                                                                                                                                      WO200175067-A2.
                                                                                                                                                                                                                                        Homo sapiens.
                                         28-OCT-1999;
29-OCT-1999;
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                                                                                                                                     RESULT 100
                                                                                                                                             ABG03470
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed considerably techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cuplypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding pattners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders cupvolpheptide and polymucleotide sequences have applications in the pulymers of data and products dependent on DNA and cand to produce other types of data and products dependent on DNA and amino acid sequences. Abgonolo-Abg30377 represent novel human diagnostic maino acid sequences Abgonolo-Abg30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in celectronic format directly from WIND at
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 33829; 103pp; English.
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Sequence 126 AA;

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Gaps
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0
; Score 25; DB 4; Length 126;
Pred. No. 2e+03;
4; Mismatches 0; Indels
100.0%;
50.0%; F
 Ouery Match
Best Local Similarity 50.0
Matches 4; Conservative
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Search completed: September 12, 2004, 02:34:00 Job time: 111 secs

probable ureidogly uncharacterized co

peptide methionine

probable integral

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                     OM protein - protein search, using sw model
                  Copyright
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September 12, 2004, 01:55:47; Search time 49 Seconds (without alignments) 15.705 Million cell updates/sec

US-09-660-302E-1 25 Perfect score:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 1 XEFIXXDX 8 Scoring table: Sequence:

hypothetical prote hypothetical prote C-phycocyanin beta shikingte kinase V dTDP-4-dehydroxham enzyme of dihydrof probable kinase fr hypothetical prote hypothetical prote hypothetical prote phypothetical prote phypothetical prote phypothetical prote precornin-6B methy hypothetical prote glycerol metabolis conserved hypothetical prote phypothetical prote glycerol metabolis conserved hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 300 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	hypothetical prote	ical 5.9K		. 2	hetical		protei				hypothetical prote		pothe	-	hypothetical prote		hypothetical 14.7K	cal	poly		probable protein-t	transcription fact	replication protei	hypothetical prote	uncharacterized co	hypothetical prote	H H	- Ca	prot
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103 104 105 106 106 100 100 100 100 100 100 100 100	11111111111111111111111111111111111111

Page 3

Query Match 100.0%; Score 25; DB 2; Length 38; Best Local Similarity 50.0%; Pred. No. 70; Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;	Qy 1 XEFIXXDX 8	:   : :       : NUCLE TERMS 7.0		RESULT 2	E45681 hypothetical 5.9K protein (gene 61.1 protein) - phage T4	N.Alternate names: gp 61.1 C.Snacies: phage M4	Lightcres: purge 14 A;Note: host Echerichia coli	C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 C:Accession: B45681: JS0562	R; Selick, H.E.; Stormo, G.D.; Dyson, R.L.; Alberts, B.M.	o. VIIO1. 67, 2303-2316, 1993 A;Title: Analysis of five presumptive protein-coding sequences clustered between the pri	A; Reference number: A45681; MUID:93188183; PMID:8383243 A: Accession: E45681	A)Status: preliminary	A;Residues: 1-54 <sel></sel>	A, Cross-references: GB:S57514; NID:g298518; PIDN:AAB25712.1; PID:g298523	Cidentics:	A.Gene: 61.1 A.Map position: 18.973-19.135	Query Match 100.0%; Score 25; DB 2; Length 54;	le+02; hes 0; Indel	Qy 1 XEFIXXDX 8		n	RESULT 3	E81922 hypothetical protein NMA0780 [imported] - Neisseria meninditidis (strain 22491 serodroup	C.Species: Neisseria meningitidis C.Date: 05-May-2000 #sequence revision 05-May-2000 #text change 02-Feb-2001	C,Accession: B81922	R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,	Nature 404, 502-506, 2000 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.	A;Reference number: A81775; MUID:20222556; PMID:10761919 A:Accession: R81922	A) Status: preliminary	A; Residues: 1-67 < PAR>	A;Cross-references: GB:ALL62/34; GB:ALL5/959; NID:g/3/3444; FIDN:CAB84063.1; FID:g/3/950 A;Experimental source: serogroup A, strain Z2491	C,Genetics: A:Gene: NMA0780	Query Match 100.0%; Score 25; DB 2; Length 67;	Similarity 50.0%; Pred. No. 1.3e+02; 4: Conservative 4: Mismatches 0: Indel	1 XEFIXXDX 8	:       ::   : 16 YEFIFPDQ			smali conserved protein, ortholog of YAAA B. subtilis CAC0003 (imported) - Clostridium a C;Species: Clostridium acetobutylicum
fructose-bisphosph fructose-bisphosph indirect positive	lysophospholipase fructose-bisphosph	conserved hypothet renlication factor	glycosyl transfera	C 4.2.3.9 aristolo	nucleoside-diphosp probable ferrochel	probable D-alanine probable fucces ev	nonstructural prot	probable oligopept hemadglutinin - in	hemagglutinin - in	hemagglutinin - in	hemagglutinin – in hemagglutinin – in	hemagglutinin - in	nemaggiucinin - in hemagglutinin - in	hemagglutinin - in	emagglutinin -	hemagglutinin - in hemagglutinin - in	probable membrane caricain (EC 3.4.2	probable periplasm	124Ul8:/ procein - probable ATPase -	conserved hypothet		proc sur1	hypothetical prote hypothetical prote	probable ABC Trans electron transfer	Į,	hemagglutinin - in fructose-bisphosph	hypothetical prote hypothetical prote	hypothetical prote hypothetical prote		S			mster led hamster)	-1997 #text_change 17-Mar-1999		<pre>ipt, gadd7, inhibits cell growth, but lacks ID:8649973</pre>			_
249 25 100.0 337 1 PAPGF 250 25 100.0 337 2 570469 251 25 100.0 337 2 F83715	25 100.0 338 2 25 100.0 338 2	25 100.0 339 2 25 100.0 340 2	25 100.0 340 2	25 100.0 342 2	25 100.0 342 2 25 100.0 346 2	25 100.0 346 2 25 100.0 346 2	25 100.0 347 1	25 100.0 347 2 25 100.0 347 2	25 100.0 347 2	25 100.0 347 2	25 100.0 347 2 25 100.0 347 2	25 100.0 347 2	25 100.0 347 2	25 100.0 347 2	25 100.0 347 2	25 100.0 347 2 25 100.0 347 2 25 100.0 347 2	25 100.0 348 2	25 100.0 348 25 100.0 350	25 100.0 353 2	25 100.0 353 2 25 100.0 353 2	25 100.0 353 2	25 100.0 356 2	25 100.0 358 2 25 100.0 358 2	25 100.0 359 2 25 100.0 360 1	25 100.0 361 2	25 100.0 362 2 25 100.0 363 2	25 100.0 363 2 25 100.0 363 2	25 100.0 363 2 25 100.0 364 2		ALIGNMENTS		KESULT 1 S68260	hypothetical protein gadd7.1 - long-tailed hamster C;Species: Cricetulus longicaudatus (long-tailed h	C;Date: 06-Dec-1996 #sequence_revision 13-Mar- C;Accession: S68260	R;Hollander, M.C.; Alamo, I.; Fornace Jr., A.: Nucleic Acids Res. 24, 1589-1593, 1996	A; Title: A novel DNA damage-inducible transcript, gadd7, A; Reference number: S68260; MUID:96211359; PMID:8649973	A;Accession: S68260 A;Status: preliminary	A;Wolecule type: mRNA A;Residues: 1-38 <hold. A;Cross_references: 1-30 &lt;</hold. 	A/CIOSB-IEIEICES: BMBL:L40430

Mon Sep 13 10:53:33 2004

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Lill protein - fruit fly (Drosophila melanogaster)
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Sep-1999
C; Accession: 862338; 862348
R; Wright, L.G.; Chen, T.; Thummel, C.S.; Guild, G.M.
J. Moll. Biol. 255, 387-400, 1996
A; Title: Molecular characterization of the 71E late puff in Drosophila melanogaster revensession: 862338
A; Reference number: 862333; MUID:96152797; PMID:8568884
A; Accession: 862338
A; Residues: 1-99 «WRL)
A; Accession: 862348
A; Accession: 86248
A; Accession: 86248
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A; Accession: 8648
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C;Genetics:
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C,Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
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                                               Indels
        Pred. No. 1.9e+02;
4; Mismatches 0;
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A;Crosa-references: FlyBase:FBgn0014850
A;Introns: 78,1
C;Superfamily: L71-10 protein
    50.0%;
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                                               4; Conservative
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89 LEFIGIDL
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C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: G37292
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Bacteriol. 183, 4825-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: C96900
C;Accession: C96900
J: Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J: Badreriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUD:21359325; PMID:21359325
A;Accession: C96900
A;Status: preliminary
A;Molecule type: DNA
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R; van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker, G
Virology 190, 587-596, 1992

A; Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compan
A; Reference number: A42955; MUD:92391075; PMID:1325697
A; Rocession: F42955
A; Molecule type: DNA
A; Residues: 1-91 < VAN>
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A;Cross-references: GB:AE001437; PIDN:AAK77990.1; PID:g15022820; GSPDB:GN00168
A;Bxperimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0003
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A,Cross-references: GB:AE001437; PIDN:AAK81130.1; PID:g15026263; GSPDB:GN00168
A)EXPERIMENTAL source: Clostridium acetobutylicum ATCC824
C;Genetics: A,Gene: CAC3193
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ES protein - human papillomavirus type 13
C:Species: human papillomavirus type 13
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Jul-1999
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C;Superfamily: papillomavirus E5 protein
C;Keywords: early protein
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Pred. No. 1.6e+02;
4; Mismatches 0;
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8 TEFIKLDS 15
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24 MEFINKDD 31
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Best Local Similarity
Matches 4; Conserv
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A;Cross-references: GB:AE004376; GB:AE003853; NID:G9657811; PIDN:AAF96329.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
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C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: D97300
R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein VCA0423 [imported] - Vibrio cholerae (strain N16961 serog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C'Accession: F82462

K;Heidelberg J. T.: Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                            - human cytomegalovirus (strain AD169)
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R;Nelson, J.A.; Fleckenstein, B.; Jahn, G.; Galloway, D.A.; McDougall, J.K. J. Virol. 49, 109-115, 1384
A;Fitle: Structure of the transforming region of human cytomegalovirus AD169.
A;Reference number: A03800; MUID:84090384; PMID:6317885
                                                                                                                                                                                                                                                                                                                        hypothetical 13K protein (transforming region) - human cytomegalovirus (stra
C,Species: human cytomegalovirus, human herpesvirus 5
C,Date: 20-Sep-1984 #sequence_revision 20-Sep-1984 #text_change 17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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C,Superfamily: human cytomegalovirus hypothetical 13K protein
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Pred. No. 2.6e+02;
4; Mismatches 0;
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Pred. No. 2.6e+02;
4; Mismatches 0;
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50.0%; P
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11 PEFIFNDN 18
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28 QEFITNDV 35
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17 AEFIALDN 24
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A;Molecule type: DNA
A;Residues: 1-119 <HEI>
                                                               1 XEFIXXDX
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A, Molecule type: DNA
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C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C; Accession: T10321 R.R. is Tunk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F. Virology 229, 381-399, 1997 A; Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosia A; Reference number: Z17011; MUID:97271300; PMID:9126251 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: DNA A; A; Multinucleocapsid nuclear polyhedrosia A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: DNA A; Multinucleocapsid nuclear DNA A; Multinucle type: DNA A; Multinucleocapsid nuclear A; A; Multinucleocapsid nuclear A; A; Multinucleocapsid nuclear A; Status: DNA A; Multinucleocapsid nuclear A; Mu
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A,Accession: G86800
A,Status: preliminary
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R; Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551
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A;Experimental source: strain O157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59051.1; PID:g1911298
C;Superfamily: Autographa californica nuclear polyhedrosis virus EcoRI-T medium protein
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A;Cross-references: GB:AE005176; PID:g12724395; PIDN:AAK05505.1; GSPDB:GN00146
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hypothetical protein Z1420 [imported] - Escherichia coli (strain O157:H7, su
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: G86800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 2; Length 109; 50.0%; Pred. No. 2.3e+02; ive 4; Mismatches 0; Indels
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Best Local Similarity 50.00
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Best Local Similarity 50.0
Matches 4; Conservative
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96 LEFIKLDV 103
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GEFIVCDE 29
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Best Local Similarity
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A,Status: preliminary
A,Molecule type: DNA
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A;Gene: Z1420
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R.J.

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hypothetical 14.7K protein - African swine fever virus
NiAlternate names: open reading frame D129L
CiSpecies: African swine fever virus, ASFV
CiDate: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jul-2000
CiDate: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jul-2000
CiDate: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jul-2000
Richards R. J.; Rodriguez, J.M.; Boursnell, M.; Rodriguez, J.F.; Vinuela, E.
Gene 134, 161-174, 1993
Afritle: Two putative African swine fever virus helicases similar to yeast 'DEAH' pre-mh
A;Reference number: JT0665; MUID:94085774; PMID:8252374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pypothetical protein Imo0151 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Spacesion: AH1093
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
D; Jones, L.M.; Karst, U.
Science 294, 849-882, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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C;Species: Enterobacter aerogenes
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T08492
R;Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
Plasmid 36, 95-111, 1996
A;Title: Conservation of the genetic switch between replication and transfer genes of In
A;Reference number: 216434; MUID:97118926; PMID:8954881
A;Accession: T08492
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-129 <YAN>
A;Cross-references: GB:U18466; NID:9780375; PIDN:AAA65332.1; PID:9780472
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50.0%; Pred. No. 3e+02;
cive 4; Mismatches
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     93 VEFIVGDD 100
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120 TEFIKIDD 127
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60 IEFIKIDP 67
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, A.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
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                                                        A;Cross-references: GB:AE001437; PIDN:AAK81191.1; PID:g15026331; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics: A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-123 <KUR>
A;Residues: 1-123 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52926.1; PID:g17983774; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C'Species: Brucella melitensis
C'Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 16-Feb-2001
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Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 4; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-124 <SCH>
A;Cross-references: EMBL:AL353821; GSPDB:GN00112; NCSP:68B2.170
A;Experimental source: cosmid contig 68B2; strain 74
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C;Superfamily: Neurospora crassa hypothetical protein 68B2.170
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50.08; F
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89 REFIHDDK 96
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GEFIVGDT 64
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                 A; Molecule type: DNA
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Best Local Similarity
Matches 4; Conserv
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A; Status: preliminary
A; Molecule type: DNA
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A;Status: preliminary
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A;Residues: 1-140 <THO>

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C;Accession: A60998
R;Walters, J.A.; Dyke, K.G.H.
FEMS Microbiol. Lett. 71, 55-64, 1990
A;Title: Characterization of a small cryptic plasmid isolated from a methicillin-resists A;Reference number: A60998
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C.Species: Caulobacter crescentus
C.Accession: A87354
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; DoBoson, R.J.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A.Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Sccssion: A87354
A;Status: preliminary
A;Molecule type: DNA
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C;Comment: This sequence represents the only long open reading frame of a small (1613 ba
                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AE000080; NID:g2182465; PID:g2182474; PIDN:AAB91730.1
A;Experimental source: strain NGR234
                                                                                                                                             C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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C;Species: Staphylococcus aureus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 10-Dec-1999
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                                                                                         transcription factor homolog Y4jR - Rhizobium sp. plasmid pNGR234a C; Species: Rhizobium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
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Pred. No. 3.4e+02;
4; Mismatches 0;
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Pred. No. 3.5e+02;
4; Mismatches 0;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-151 <FRE>
                                                                                                                                                                                                 R;Freiberg, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: 220492
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C;Superfamily: plasmid replication protein REP
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50.0%; F
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Best Local Similarity 50.0
Matches 4; Conservative
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PEFIILDM 54
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A;Residues: 1-154 <WAL>
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13 EEFINKDS
                                                                                                                                                                       C, Accession: T28645
R; Freiberg, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: y4jR
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                                     RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                  RESULT 20
G97212
C) Forbable acetyltransferase [imported] - Clostridium acetobutylicum
C) Species Clostridium acetobutylicum
C) Species Clostridium acetobutylicum
C) Species Clostridium acetobutylicum
C) Species Clostridium acetobutylicum
C) Baccession: G97212
C) Rocession: G97212
C) Rocession: G97212
C) Romin, B.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N., Roonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A) Rittle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A) Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable protein-tyrosine-phosphatase (EC 3.1.3.48) Cjl258 [imported] - Campylobacter je probable protein-tyrosine-phosphatase (EC 3.1.3.48) Cjl258 [imported] - Campylobacter je c) Species: Campylobacter jejuni compylobacter jejuni alimar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002 CjAccession: D8133 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin Nature 4031, 665-668, 2000 A; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyperference number: A81250; MUID:20150912; PMID:10688204
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A;Cross-references: GB:AL139077; GB:AL11168; NID:g6968444; PIDN:CAB73512.1; PID:g696869
A;Experimental source: serotype O2, strain NCTC 11168
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A/Status: preliminary
A/Molecule type: DNA
A/Molecule type: DNA
A/Residues: 1-149 «KUR»
A/Cross-references: GB:AE001437; PIDN:AAK80490.1; PID:g15025561; GSPDB:GN00168
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC2539
A;Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64436.1; PID:g1572541
C;Genetics:
A;Gene: tnpA
A;Genome: plasmid R751
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A;Gene: Cj1258
C;Superfamily: protein-tyrosine-phosphatase, low molecular weight
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                             Length 140;
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                                                                                                                                    ; Score 25; DB 2; Length 14
Pred. No. 3.1e+02;
4; Mismatches 0; Indels
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50.0%; P
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Best Local Similarity 50.0
Matches 4; Conservative
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51 LEFIVIDV 58
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24 LEFITGDS 31
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Best Local Similarity
Matches 4; Conserva
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A, Status: preliminary
A; Molecule type: DNA
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AG1755

AG1755

Bacteriophage protein homolog lin2588 [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua

C;Species: Listeria innocua

C;Species: Listeria innocua

C;Accession: AG1755

R;Adlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke

R;Adlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bibli, H

D; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M

A;Authors: Kreft, J.; Kuhn, M.; Rust, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M

A;Title: Comparative genomics of Listeria species.

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Status: preliminary

A;Residues: L-160 < GLA>

A;Cross-references: GB:AL552022; PIDN:CAC97815.1; PID:g16415125; GSPDB:GN00178

A;Gene: Lin2588

C;Superfamily: Streptococcus phage phi-O1205 hypothetical protein 11
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Pypotherical protein BH1868 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C;Accession: D83883

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir
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50.0%; Pred. No. 3.6e+02;
ive 4; Mismatches 0; Indels
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Pred. No. 3.6e+02;
4; Mismatches 0;
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26 REFIAQDR 33
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Cispecies: CACO166
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C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Avariety PCC 6803
C;Accession: S76232
C;Accession: Accession: Accessi
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A; Residues: 1-157 < KAN>
A; Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18491.1; PID:g165357
A; Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18491.1; PID:g165357
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Genetics:
A; Start codon: GTG
C; Superfamily: Synechocystis hypothetical protein s110272
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A;Cross-references: GB:AE005673; NID:g13422099; PIDN:AAK22829.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0844
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A;Accession: S76232
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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ilarity 50.0%; Pred. No. 3.5e+02;
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123 VEFIENDI 130
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39 TEFINODF 46
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100.0%;

Similarity 50.0 4; Conservative

Query Match Best Local S: Matches 4

A;Gene: BH1868

REFIRIDI 18 1 XEFIXXDX 8

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A;Cross-references: GB:AL591985; PIDN:CAC49567.1; PID:g15141054; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
B;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Coines, T.
L.; Hyman, R.W.; Jones, T.
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, Hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.Affitle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                               RibelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, B.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes: Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten: A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 24.Aug-2001 #sequence_revision 24.Aug-2001 #text_change 14.Sep-2001 C;Accession: G55987  
E;Accession: G55987  
E;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc. A;Reference number: A95842; MUID:21396508; PMID:11481431
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A; Residues: 1-167 < KUR>
A; Cross-references: GB: AE008917; PIDN: AAL52248.1; PID: g17983034; GSPDB: GN00190
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                  Gaps
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               Pred. No. 3.7e+02;
4; Mismatches 0;
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Pred. No. 3.8e+02;
4; Mismatches 0;
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4; Mismatches 0;
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               50.08;
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105 DEFIIKDF 112
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SEFIVADN 64
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               Similarity
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A,Molecule type: DNA
A,Residues: 1-170 <KUR>
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                                                                                                                                                                                                            A;Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB05587.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
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A;Residues: 1-164 <PAR>
A;Cross-references: GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73419.1; PID:g696859
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
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A;Cross_references: GB:AE002125; GB:AF222894; NID:g6899253; PIDN:AAF30698.1; GSPDB:GN001
Nucleic Acids Res. 28, 4317-4331, 2000
A/TLLE: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Status: preliminary
A/MACESION: D83883
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A/MACESION: D83883
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50.0%; Pred. No. 3.7e+02;
live 4; Mismatches 0; Indels
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Pred. No. 3.7e+02,
4; Mismatches 0, Indels
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A;Gene: Cj1165c C;Superfamily: primosomal operon 14K protein

A, Accession: G81321 A, Status: preliminary A, Molecule type: DNA

Conservative

Best Local Similarity Matches 4; Conserv

Query Match

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Db

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C;Superfamily: peptide methionine sulfoxide reductase

A; Genetic code: SGC3

Query Match

A; Gene: msrA; UU289

C; Genetics:

A; Experimental source: serovar 3; biovar

A;Status: preliminary A;Molecule type: DNA

A; Accession: G82910

100.0%; Score 25;

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A;Status: preliminary
A;Status: Dreliminary
A;Molecule trype: DNA
A;Molecule trype: DNA
A;Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB07650.1; GSPDB:GN0
A;Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB07650.1; GSPDB:GN0
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A; Molecule type: DNA
A; Residues: 1-172 < DELA
A; Cross-references: GB: K02660; NID: g142182; PIDN: AAB05343.1; PID: g142183
A; Experimental source: strain PR-6
B; Pilot, T.-1; Fox, J.L.
Proc. Natl. Acad. Sci. U.S.A. 81, 6983-6987, 1984
A; Title: Cloning and sequencing of the genes encoding the alpha and beta subua A; Reference number: A94017; MUD: 85063716; PMID: 6438628
A; Note: Agmental undaruplicatum
A; Accession: B94017
A; Molecule type: DNA
A; Residues: 1-172 < PILD
A; Cross-references: GB: K02659; NID: g142176; PIDN: AAB05341.1; PID: g142177
A; Experimental source: strain PR-6
C; Superfamily: phycocyanin
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C;Species: Synechococcus sp.
C;Species: Synechococcus sp.
C;Date: 13-Aug-1986 #text_change 11-Jun-1999
C;Accession: B94024; B94017; A0321; A22972
R;de Lorimier, R.; Bryant, D.A.; Porter, R.D.; Liu, W.Y.; Jay, E.; Stevens JProc. Natl. Acad. Sci. US.A. Bl., 746-7950, 1984
A;Title: Genes of the alpha and beta subunits of phycocyanin.
A;Reference number: A94024; MUID:85088525; PMID:6096868
A;Note: Agmenellum quadruplicatum
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50.0%; Pred. No. 3.9e+02;
iive 4; Mismatches 0; Indels
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Pred. No. 3.9e+02;
4; Mismatches 0;
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137 NEFIVMDS 144
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GEFISSDK 23
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                                                                                                                                                                                                                                                   Uncharacterized conserved protein CAC1676 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #text_change 14-Sep-2001 R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G37106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170 cKUR>
A;Residues: 1-170 cKUR>
A;Residues: 1-170 cKUR>
A;Residues: Clostridium acetobutylicum ATCC824
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C84141
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C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Accession: E71530
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A;Reference number: A71570; MUID:99000809; PMID:9784136
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A;Cross-references: GB:AE001303; GB:AE001273; NID:g3328718; PIDN:AAC67896.1; PID:g332871
A;Experimental source: serotype D, strain UM-3/Cx
C;Genetics:
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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5 REFIGADV 12
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50 LEFIDNDY
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probable kinase from adenilate kinase family, FLAR-like protein [imported] - Clostridium (Species: Clostridium acetobutylicum (CiSpecies: Clostridium acetobutylicum (CiSpecies: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 (CiAccession: H97205 Fivelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee J. Daly, M.J.; Bannett, G. M.; Koonin, B.V.; Smith, D.R. Asteriol. 183, 4823-4838, 2001 A; File: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Classification of the Mulder: A96900; MUID:21359325; PMID:21359325
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Accession: A64300; MUID:96337999; PMID:8688087
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A,Cross-references: GB:AE001437; PIDN:AAK80435.1; PID:g15025501; GSPDB:GN00168
A,Experimental source: Clostridium acetobutylicum Arcc824
C;Genetics:
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: A64393
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr_2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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C;Superfamily: hypothetical protein MJ0745
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50.0%; F
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23 SEFIITDD 30
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A;Experimental source: Serogroup O1; Strain N16361; biotype El Tor C;Genetics: Ashar CC (C) Strain N16361; biotype El Tor Ashar (C) Strain N16361; biotype El Tor C;Genetics: A;Gene (C) Strain N16361; biotype El Tor C) Strain N16461; biotype El Tor C) Strain N16461
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Cibate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
Cipate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
Cipate: 14-Sep-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme of dihydrofolate reductase family, ortholog YWFD B. subtilis [imported] - Clostri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dTDP-4-dehydrorhamnose 3,5 epimerase (rfbC-2) [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Accession: 690357
R;She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90357
A;Accession: G90357
A;Status: preliminary
A;Molecule type: DNA
A;Residues: I-176 <KUR>
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A;Notatus: preliminary
A;Molecule type: DNA
A;Residues: 1-176 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK79463.1; PID:g15024442; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
A;GeneticsCAC495
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C;Superfamily: shikimate kinase; shikimate kinase homology
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C;Superfamily: dTDP-4-dehydrorhamnose 3,5-epimerase
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50.0%; Pred. No. 4e+02;
cive 4; Mismatches
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Pred. No. 4e+02;
4; Mismatches
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KEFIISDK 162
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30 MEFIDSDT 37
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Best Local Similarity
Matches 4; Conserva
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Best Local Similarity
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Dybocosystem I chain III - Odontella sinensis chloroplast
NiAlternate names: photosystem I plastocyanin-binding chain
C;Species: chloroplast Odontella sinensis
C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 20-Jun-2000
C;Accession: S78329
R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Itle: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sinens
A;Reference number: S7828
A;Accession: S78329
A;Accession: S78329
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-185 <KOW>
A;Cross-references: EMBL:Z67753; NID:g1185127; PIDN:CAA91702.1; PID:g1185219
A;Cross-references: EMBL:Z67753; NID:g1185127; DIDN:CAA91702.1; PID:g1185219
C;Genetics:
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By Cotherical protein MTH578 - Methanobacterium thermoautotrophicum (strain Delta H)

Cipecies: Methanobacterium thermoautotrophicum

Kisinith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Kimith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Kinith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Kisinith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Reeve, J.N.

Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

A.Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A,Reference number: A69000; MUID:98037514; PMID:9371463

A,Reference number: A69000; Mulpissender end shown; translation not shown

A,Molecule type: DNA

A,Residues: L-186 < ATHAN-ARAB85084.1; PIDN:AAB85084.1; PIDS:G26216
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A;Experimental source: strain Delta H
C;Genetics:
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C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 18-Aug-2003
C;Accession: 697069
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Genome : chloroplast
C;Superfamily: photosystem I chain III
C;Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem I
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100.0%; Score 25; DB 2; Length 18
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 4; Mismatches 0; Indels
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122 DEFIIQDE 129
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71 VEFISGDV 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein APE1503 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H72630
C;Accession: H72630
B;Kawarabayasi, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Vamazaki, J.; R
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyx
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72630
A;Status: preliminary
A;Accessidues: DNA
A;References: DNA
A;Cross-references: DDBJ;AP000061; NID:95104821; PIDN:BAA80502.1; PID:d1044288; PID:9510
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Accession: C83913
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05826.1; GSPDB:GN00
A;Experimental source: strain C-125
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Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
Accession: C83913
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50.0%; Pred. No. 4.2e+02;
iive 4; Mismatches 0;
                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-181 <BEV>
A;Cross-references: EMBL:AL162508
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C, Genetics:
A, Gene: APE1503
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Best Local Similarity 50.0%
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Best Local Similarity 50.00
Matches 4; Conservative
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121 MEFIYHDS 128
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Best Local Similarity
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          A;Accession: T48241
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A; Introns: 158/1
A; Note: T7H20.250
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100.0%; Score 25; DB 2; Length 18 50.0%; Pred. No. 4.38+02; ive 4; Mismatches 0; Indels

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C; Superfamily: precorrin-6Y methylase CbiT

C;Genetics: A;Gene: CAC1378

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A, Molecule type: DNA
A, Residues: 1-192 <br/>
A, Molecule type: DNA
A, Residues: 1-192 <br/>
A, Residues: 1-192 <br/>
A, Residues: 1-192 <br/>
A, Cross-references: GB: Moszer, I.; Albertin; A: M: Alloni, G.; Azevedo, V.; Berte: G.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch. A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle: Inch, J.; Harwod, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee, Y.; M.; Ogdwar, K.; Oglwara, A.; Oglwara, B.; Park, S.H.; Parro, V.; Pohl; T.M.; Portetell, R; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, P.; Schroeter, P.; Schroeter, P.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamanoto, H.; Yamanoto, K.; Yata, K.; Yata, K.; Yata, K.; Yoshida, J. A; Reference number: A69580; MulD:98044033; PMID:9384377
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A;Experimental source: strain 168
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I Exage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: B47700; D69634
R;Beijer, L.; Milson, R.P.; Holmberg, C.; Rutberg, L.
J. Gen. Microbiol. 139, 349-359, 1993
A;Title: The glpp and glpF genes of the glycerol regulon in Bacillus subtilis.
A;Reference number: A47700; MUID:93171878; PMID:8436953
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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C;Keywords: transcription antitermination; transcription regulation
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tive 4; Mismatches 0;
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Apothetical protein BB0001 - Lyme disease spirochete
C'Species: Borrelia burgdorferi (Lyme disease spirochete)
C'Species: Bornelia burgdorferi (Lyme disease spirochete)
C'Species: B
Jaly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A.Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97069
A;Accession:
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A,Cross-references: GB:AE001115; GB:AE000783; NID:g2687879; PIDN:AAC66406.1; PID:g268789
A,Experimental source: strain B31
C,Superfamily: Borrelia burgdorferi hypothetical protein BB0001
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C;Genetics:
A;Gene: RC0043
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A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID: 98065943; PMID: 9403685
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C; Superfamily: hypothetical protein H10304

Conservative

4;

Local Similarity

Query Match

:|||::|: 156 KEFIFADN 163

qq ò

1 XEFIXXDX 8

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100.0%; Score 25; DB 2; Length 190;
  Query Match
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A; Accession: A70100

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probable regulator [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050995 C;Species: Escherichia coli C;Date: 18-Jul-2001 C;Date: 18-Jul-2001 Escherichia coli C;Date: 18-Jul-2001 Escherichia coli C;Date: 18-Jul-2001 Escherichia coli C;Date: 18-Jul-2001 Escherichia coli Diashi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res: 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench, Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: D90669 A;Accession: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable regulator ykgK [imported] - Escherichia coli (strain 0157:H7, substrain EDL933 C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: G85519
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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A,Status: preliminary
A,Molecule type: DNA
A,Rosiduse: 1-196 <STO>
A,Essiduses: 1-196 <STO>
A,Experimental source: strain O157:H7, substrain EDL933
C,Genetics: A,Gene: ykgK
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c;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: F64755
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
A; Rose, D.J.; Mau, B.; Shao, Y.
A; Rose, D.J.; Mau, B.; Shao, Y.
A;Title: The complete genome sequence of Escherichia coli K-12.
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50.0%; Pred. No. 4.5e+02;
iive 4; Mismatches 0; Indels
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Pred. No. 4.5e+02;
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4; Mismatches
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50.0%; E
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Best Local Similarity 50.0
Matches 4; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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93 GEFIEGDK 100
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72 TEFINRDN 79
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72 TEFINRDN 79
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1 XEFIXXDX 8
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R;Agostoni Carbone, M.L.; Panzeri, L.; Melchioretto, P.; Carignani, G.; Feroli, F.; Fron
submitted to the Protein Sequence Database, May 1996
A;Reference number: 864577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein At2940440 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84829
R;Lin, X:, Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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A;Residues: 1-196 <AGO>
A;Cross-references: EMBL:273036; NID:g1323455; PID:e243683; PID:g1323456; GSPDB:GN00007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Séquence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUD:20083487; PMID:10617197
A;Accession: E84829
A;Statuus: preliminary
A;Molecule type: DNA
A;Residues: 1-194 <STO>
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N;Alternate names: hypothetical protein G9140
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
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Pred. No. 4.5e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                              Length 192;
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Pred. No. 4.4e+02;
4; Mismatches 0;
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50.0%; F
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A;Map position: linear chromosome
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A;Map position: 7R
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Best Local Similarity 50.v..
A; Conservative
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159 DEFIVGDD 166
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                                          A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-192 <KUR>
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          A; Accession: AD3014
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A; Map position: 2
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Ridlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Meok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUD:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Liŝteria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AH1169
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
                                                                                                                                                                                                                                           hypothetical colled-coil protein [imported] - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                               C, Accession: T50322
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Cadieu, E.; Lelaure, V.; Galibert, submitted to the EMBL Data Library, January 2000
A;Reference number: Z25061
A;Reference number: Z25061
A;Reference number: Z25061
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-202 AMD>
A;Residues: 1-202 AMD>
A;Cross-references: EMBL:AL136536; PIDN:CAB66453.1; GSPDB:GN00067; SPDB:SPBC1703.09
A;Experimental source: strain 972h(-); cosmid c1703
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A)Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein lin0754 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AB1527
                                                                                                                                                                                                                                                                                       C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
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Pred. No. 4.7e+02;
1; Mismatches 0; Indels
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Pred. No. 4.7e+02;
1; Mismatches 0; Indels
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50.0%; E
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50.0%; E
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TEFIPADV 45
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-202 <GLA>
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44 NEFILIDE
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N.Alternate names: hypothetical protein C09_orf201

C;Species: Mycoplasma pneumoniae protein C09_orf201

C;Species: Mycoplasma pneumoniae A;Variety: ATCC 29342

A;Variety: ATCC 29342

C;Accession: S73365

R;Himmelreich, R:; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A;Ntle: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A;Neference number: S73327; MUID:97105885; PMID:8948633

A;Accession: S73365

A;Accession: S73365

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Regidues: L-201 #HIMS

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                                                                                                                                                                                           A;Cross-references: GB:AE000136; GB:U00096; NID:g2367103; PIDN:AAC73397.1; PID:g2367106;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
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                                       A;Accession: F64755
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-196 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C;Accession: T027AP
R;Lorbiecke, R.; Sauter, M.
Submitted to the EMBL Data Library, February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AF050200; NID:g2952337; PID:g2952338
C;Genetics:
A;Gene: SIP2
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 25; DB 2;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: Z14738
A;Accession: T02787
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Query Match
Best Local Similarity 50.0
Matches 4; Conservative

1-199 <LOR>

A; Residues:

:|||::|: 34 KEFIPVDK 41

1 XEFIXXDX 8

à Db

probable submergence induced protein 2 - rice

RESULT 58

:|||::|: 72 SEFINRDN 79

1 XEFIXXDX 8

ð g

A;Gene: ykgK

A;Cross-references: EMBL;AE000005; GB:U00089; A;Note: the nucleotide sequence was submitted

A;Gene: infC A;Genetic code: SGC3

4; Conservative

1 XEFIXXDX 8

Query Match Best Local Similarity Matches 4; Conserva

0;

Gaps

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hypothetical protein AGR_L_2230 [imported] - Agrobacterium tumefaciens (strain C58, Cer
A; Cross-references: GB: U67494; GB: L77117; NID: 91591120; PIDN: AAB98415.1; PID: 91591133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteinase B (EC 3.4.23.-) - fungus (Scytalidium lignicolum)
C;Species: Scytalidium lignicolum
C;Species: Scytalidium lignicolum
C;Species: Scytalidium lignicolum
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 31-Dec-1993
C;Accession: A28864
R;Maita, T.; Nagata, S.; Matsuda, G.; Maruta, S.; Oda, K.; Murao, S.; Tsuru, D.
A;Title: Complete amino acid sequence of Scytalidium lignicolum acid protease B.
A;Reference number: A28864; MUID:84185536; PMID:6370989
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50.0%; Pred. No. 4.8e+02;
ive 4; Mismatches 0; Indels
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Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 4; Mismatches 0;
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llarity 50.0%; Pred. No. 4.8e+02;
Conservative 4; Mismatches 0,
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A,Residues: 1-204 <MAI>
C,Keywords: aspartic proteinase; hydrolase
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A;Gene: PA4671
C;Superfamily: 508 ribosomal protein L25
                                                                                                 A, Map position: REV386963-386349
C, Superfamily: dCTP deaminase
C, Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
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144 PEFIEVDM 151
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38 DEFIIYDD 45
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C;Species: Listeria innocua
C;Date: 27-Nov-2001
C;Date: 27-Nov-2001
C;Accession: AC1595
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshii, H.D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kunn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matchors: Kreft, J.; Kunn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1595
A;Accession:
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A.Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A.; Aithers Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A.Recession: F64353
A.Accession: F64353
A.Accession: F64353
A.Accession: preliminary; nucleic acid sequence not shown; translation not shown
A.Residues: 1-204 <BUL>
                  D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title. Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Status: Dreliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:NC_003210; PIDN:CAC98838.1; PID:g16410149; GSPDB:GN00177
A;Cxperimental source: strain EGD-e
A;Genetics:
A;Genetics:
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A;Coss-references: GB:AL592022; PIDN:CAC96531.1; PID:g16413773; GSPDB:GN00178
A;Cxoss-references: GB:AL592022; PIDN:CAC96531.1; PID:g16413773; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics: A;Genetics: A
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
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Pred. No. 4.7e+02;
4; Mismatches 0; Indels
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50.0%; P
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Best Local Similarity 50.03
Matches 4; Conservative
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57 NEFIVRDQ
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probable glutathione S-transferase protein [imported] - Sinorhizobium mellioti (strain C;Species: Sinorhizobium mellioti
C;Species: Sinorhizobium mellioti
C;Species: Sinorhizobium mellioti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 02-Aug-2002
C;Accession: F95892
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna: Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing end: A;Accession: F95892
A;Accession: F95892
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Ryanonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 200
AyTitle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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RGalibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Candin, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F., L.; Hyman, R.W.; Jones, T.

L.; Hyman, R.W.; Jones, T.

A; Science 293, 668-572, 2001

A; Atuthors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weils, D.H.; Wong, K.; Yeh, K.A; Rieference number: A96039; MUID:21368234; PMID:11474104
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A,Experimental source: strain 9a5c
B,Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laign
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Dec-2002
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Pred. No. 4.8e+02;
4; Mismatches 0;
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C;Superfamily: hypothetical protein b0838
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-208 <SIM>
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C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: C98270
C;Accession: C98270
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 244, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Recession: C98270
A;Accession: C98270
A;Cross-references: GB.AE007870; PIDN:AAK89685.1; PID:g15159591; GSPDB:GN00170
C;Genetics:
A;Gene: AGR L_2230
A;Map position: linear chromosome
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A:Experimental source: strain Madrid E
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C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C;Accession: E97825
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
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A;Reference number: A97700; MUID:21442074; PMID:11557893
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50.0%; Pred. No. 4.8e+02;
iive 4; Mismatches 0;
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A;Gene: rplD; RP658
C;Superfamily: Bscherichia coli ribosomal protein L4
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A,Gene: rplD
C,Superfamily: Escherichia coli ribosomal protein L4
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172 DEFIVGDD 179
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VEFIRDDI 32
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A;Status: preliminary
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A,Cross-references: GB:AE006914; PIDN:AAL03858.1; PID:g15620461; GSPDB:GN00173
C;Genetics:
A;Gene: RC1320
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A;Molecule type: DNA
A;Residues: 1-209 <KUR>
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C;Species: Dacesion: I40484; A69729; S49364
R;Martinussen, J.;Glaser, P.; Andersen, P.S.; Saxild, H.H.
J; Bacteriol. 177; 271-274, 1995
A;Title: Two genes encoding uracil phosphoribosyltransferase are present in Bacillus sub
A;Reference number: 140473; MUID: 95095982; PMID: 7798145
A;Accession: 140484
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocassion: 140484
A;Residues: 1-209 *RES>
A;Residues: 1-209 *RES>
A;Residues: EMBL: 238002; NID: 9556877; PIDN: CAA86111.1; PID: 9556887
A;Rossidues: EMBL: S38002; NID: 9556877; PIDN: CAA86111.1; PID: 9556887
A;Rossidues: EMBL: S38002; NID: 956877; PIDN: CAA86111.1; PID: 9556887
A;Rossidues: EMBL: S38002; NID: 956877; PIDN: CAA86111.1; PID: 956887
A;Runst, P:; Ogaaswara, N:; Moszer, I:; Albertini, A.M.; Alloni, G:; Azevedo, V.; Carter, C.; Brunt, S.; Brunschi, C.Y.; Caldwell, B.; Capuano, V.; Carter, C.; Rerington, J.; Fabret, C.; Furita, M.; Fujita, M.; F
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa. R.G.; Santelli, R.V.; Sawasak A, Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; Bilveira Silva, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z., Contents: annotation
C;Genetics:
A;Gene: XF2643
C;Superfamily: 50S ribosomal protein L25
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, Bubmitted to the Protein Sequence Database, September 1999
A;Accession: T17329
A;Accession: T17
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A;Experimental source: fetal brain; clone DKFZp564K2364
C;Genetics:
A;Note: DKFZp564K2364.1
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159 VEFIRHDR 166
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144 PEFIEVDL 151
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akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Authors: Yoshikawa, H.; Danchin, A.
A., Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A., Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A., Accession: A69729
A., Accession: A69729
A., Accession: A69729
A., Residues: DNA
A., Residues: 10.209 < KUN>
A., Cross-references: GB: 299122; GB: AL009126; NID: G2636029; PIDN: CABIS706.1; PID: G2636214
A., Experimental source: strain 168
C., Genetics:
A., Genetics:
A., Genetics:
A., Genetics: A., Genetics: GB: Allowed Complex of the C
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C;Species Rickettsia prowazekii a d the origin of mitochondria.
R;Andersson, S(G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: C71647
A;Accession: C71647
A;Accession: C71647
A;Accession: C71647
A;Residues: 1-209 cAND>
A;Residues: 1-209 cAND>
A;Residues: 1-209 cAND>
A;Cross-references: GB:AJ235273; GB:AJ235269; NID:93861237; PIDN:CAA15275.1; PID:938613
A;Gene: RP851
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50.0%; Pred. No. 4.9e+02;
cive 4; Mismatches 0; Indels
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125 REFIVVDP 132
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D.; R

Length 209; Score 25; DB 2; Pred. No. 4.9e+02; 100.0%; Best Local Similarity

Matches

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A;Accession: S28955
A;Molecule type: mRNA
A;Residues: 1-210 <ABA.
A;Cross-terences: EMBL:X65868; NID:g4973; PIDN:CAA46698.1; PID:g4974
C;Superfamily: dTMP kinase
C;Keywords: ATP; nucleotide binding; nucleotide biosynthesis; P-loop; phosphotransferase
F;14-21/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: preliminary
  R,Abaigar, L.T.; Yeh, Y.I.S.; Jong, A.Y.
Biochim. Biophys. Acta 1132, 222-224, 1992
A;Title: Functional and structural conservation of Schizosaccharomyces pombe dTMP kinas:
A;Reference number: S28955; MJID:93003330; PMID:1327149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiDate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
CiAccession: A85098
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Colo Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
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A;Moleoule type: DNA
A;Residues: 1-211 «SITO»
A;Cross-references: GB:NC_001268; NID:g7267654; PIDN:CAB78082.1; GSPDB:GN00140
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Similarity 50.0%; Pred. No. 4.9e+02;
4; Conservative 4; Mismatches 0; Indels
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Pred. No. 4.9e+02;
4; Mismatches 0;
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Pred. No. 4.9e+02;
4; Mismatches 0;
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50.08; F
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LEFITLDA 182
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PEFILQDT 56
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C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C.Accession: E89009
R.anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A.Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A.Reference number: A75000; MUID: 99069613; PMID: 99853916
A.Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleA.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A.Status: preliminary
A.Molecule type: DNA
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Accession: T41553
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D. submitted to the EMBL Data Library, June 1998
A;Reference number: Z22001
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dTMP kinase (EC 2.7.4.9) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 06.Feb-1995 #sequence_revision 06.Feb-1995 #text_change 19-Jan-2001
C:Accession: S28955
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Pred. No. 4.9e+02;
4; Mismatches 0; Indels
     Indels
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50.0%; Pred. No. 4.9e+02;
tive 4; Mismatches 0;
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%Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-210 <WOO>
  Mismatches
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4; Conservative
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LEFIQCDA 164
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C;Superfamily: dTMP kinase
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LEFITLDA 183
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69 IEFIDADY 76
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A;Gene: SPDB:SPCC70.07c
A;Map position: 3
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Best Local Similarity
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RESULT 78

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A; Map position: 5

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C;Genetics: A;Gene: R08E5.1

A; Residues:

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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: E82675
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: E82675
A;Atlie: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUDD: 20365717; PMID: 10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Rederence number: A82515; MUDD: 20365717; PMID: 10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Reducs: preliminary
A;Note: for a complete list of authors see reference number A59328 below
A;Residues: 1-213 <SIM>A;Residues: 1-213 <SIMAA;Residues: 1-
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C,Species: Borrelia burgdorferi (Lyme disease spirochete)
C,Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Dec-2002
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Pred. No. 5e+02;
4; Mismatches
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Best Local Similarity 50.03
Matches 4; Conservative
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172 PEFIELDL 179
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                               scytalidopepsin B (EC 3.4.23.32) precursor - fungus (Scytalidium lignicolum) (fragment) NiAlternate names: pepstatin-insensitive acid; scytalidium aspartic proteinase B C.Species: Scytalidium lignicolum nignicolum (C.Species: Scytalidium lignicolum lignicolum (C.Species: Scytalidium lignicolum (C.Species: Scytalidium lignicolum (C.Species: Scytalidium lignicolum (C.Species: Scotachol: Biochem: 60, 1210-1211, 1996
A.Title: Nucleotide sequence of the gene encoding pepstatin-insensitive acid protease B, A;Rocession: UC4883; MUD:96376187; PMD:8782420
A.Reference number: JC4883; MUD:96376187; PMD:8782420
A.Residues: 1-211 - KA1>
A.Cocession: PC4182
A.Molecule type: Drotein
A.Molecule type: protein
A.Molecule type: protein
A.Residues: 1-211 - KA2>
C.Comment: This enzyme is insensitive to pepstatin.
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Cispecies: Pseudomonas aeruginosa
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Cispecies: Pseudomonas aeruginosa
Cispecies: Pseudomonas aeruginosa
Cipace: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
Ciacession: A83521
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
A;Reference number: A82550; MUID:20437337; PMID:10984043
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A,Cross-references: GB:AE004532; GB:AE004091; NID:g9946896; PIDN:AAG04379.1; GSPDB:GN001
A,Experimental source: strain PA01
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E82675
hypothetical protein XF1489 [imported] - Xylella fastidiosa (strain 9a5c)
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136 AEFIIEDF 143
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PEFILQDT 56
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Best Local Similarity
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Gaps

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uridylate kinase (pyrH) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Becies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2003
C;Accession: A6505.
C;Accession: A6505.
C;Accession: A6505.
C;Accession: A6505.
C;Accession: A6505.
C;Accession: A6505.
C;Becieved 18-Aughors: K.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.
C; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Attle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MuID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: D91079
E;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F
surfett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
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A;Cross-references: GB:AE000962; GB:AE000782; NID:g2689285; PIDN:AAB89213.1; PID:g264849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE006641; NID:g13813505; PIDN:AAK40691.1; GSPDB:GN00155 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SSO0361 [imported] - Sulfolobus solfataricus
                                                                                                                                                                                                               Length 218;
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                                                                                                                                                                          Score 25; DB 2; Length 210
Pred. No. 5.1e+02;
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                    A; Experimental source: cultivar Columbia
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50.0%; E
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C;Superfamily: uridylate kinase
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Matches 4; Conservative
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177 NEFIFSDS 184
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124 AEFIKADV 131
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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A; Residues: 1-218 < KUR>
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                                                    C,Genetics:
A,Gene: TINY
A,Map position: 5
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: E6939
C;Accession: E693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutathione transferase (EC 2.5.1.18) homolog GST1 - potato
N.Alternate names: glutathione S-transferase, pathogenesis-related protein prpl-1
C;Species: Solanum tuberosum (potato)
C;Pate: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999
R;Strittmatter, G.
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A,Accession: T07595
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-217 <STR>
A,Residues: 1-217 <STR>
A,Cross-references: EMBL:J03679; NID:g862344; PIDN:AAA68430.1; PID:g169549
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A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-218 <HUA>
A;Cross-references: EMBL:AC005405; NID:g3406034; PID:g3406035
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40 AEFIRADV 47
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29 YEFIEEDL 36
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A;Gene: gstl A;Introns: 103/3

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Matches

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Gaps

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Dypothetical protein Imo2166 (imported) - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AF1345
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
R;Glaser, P.; Frangeul, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
A;Authors: Kreft, J.; Sumose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AF1345
A;Accession: AF1345
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N;Alternate names: orfl protein
N;Alternate names: orfl protein
N;Alternate names: orfl protein
C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 24-Nov-1999
C;Accession: A29891; A34765; A44221; H72851
J; Nirol. 62, 463-471, 1988
A;Title: Functional mapping of Autographa californica nuclear polyhedrosis virus genes A;Reference number: A93041; MJID:88091055; PMID:2826808
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A;Molecule type: DNA
A;Cross-references: EMBL:M18857; NID:g332482; PIDN:AAA66808.1; PID:g808753
B;O'Reilly, D.R.; Passarelli, A.L.; Goldman, I.F.; Miller, L.K.
J. Gen. Virol. 71, 1029-1037, 1990
A;Title: Characterization of the DA26 gene in a hypervariable region of the Autographa
A;Reference number: A34765; MUID:90264832; PMID:2189022
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A;Residues: 1-225 <OAR>
A;Cross-references: GB:M22619; GB:M33904; NID:g332422; FIDN:AAA69846.1; PID:g896308
A;Ersunagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.
Virology 191, 1003-1008, 1992
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A,Experimental source: strain EGD-e
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A;Molecule type: DNA
A;Residues: 1-222 <HAY>
A;Residues: 1-22 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB35697.1; PID:g13361740; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECS2274
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Pred. No. 5.2e+02;
4; Mismatches 0;
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50.08; F
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171 KEFILPDE 178
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54 VEFIGODG 61
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                                                    hypothetical protein CAC0987 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession. H97021
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Barteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA, Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno A;Acession: B90913
A;Accession: B90913
A;Status: preliminary
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R,Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0987
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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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.larity 50.0%; Pred. No. 5.2e+02;
Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25, DB 2, Length 22
Pred. No. 5.2e+02,
4; Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-2-2-4HEI>
A;Cross-references: GB:AE004102; GB:AE003852; NID:g9654512; A;Experimental source: serogroup Ol; strain N16961; biotype 1; C;Genetics: A;Gene: VCO113
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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124 KEFISIDL 131
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208 LEFIGNDV 215
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-221 <KUR>
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Best Local Similarity
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A;Status: preliminary
A;Molecule type: DNA
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Riclaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker. D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karet, U. Science 294, 849-852, 2001
Aphathors: Krefer, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makhatle. Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
           ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1477
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C;Bate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: D90057
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Miautani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:NC_003210; PIDN:CAD00855.1; PID:g16409692; GSPDB:GN00177 A;Experimental source: strain EGD-e C;Genetics:
                                                                                                                                                                                                                                                                 A;Cross-references: GB:AL592022; PIDN:CAC95586.1; PID:g16412782; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein lmo0328 [imported] - Listeria monocytogenes (strain EGD-e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/Status: preliminary
A/Status: preliminary
A/Modecule type: DNA
A/Residues: 1-226 < XUR>
A/Cross-references: GB:BA000018; PID:gl3702481; PIDN:BAB43622.1; GSPDB:GN00149
A/Experimental source: strain N315
A/Genetics:
A/Gene: SA2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein SA2319 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Listeria monocytogenes
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Pred. No. 5.3e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 5.36
4, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
50.0%;
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IEFIGEDT 113
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106 IEFIGEDT 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                     A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-226 <GLA>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-226 <GLA>
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Matches 4; Conserv
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AB1477
hypothetical protein lin0353 [imported] - Listeria innocua (strain Clip11262)
C.Species: Listeria innocua
C.Species: Z7-Nov-2001
C.Species: Z7-Nov-2001
C.Species: Z7-Nov-2001
C.Species: Z7-Nov-2001
S.Species: Z7-Nov-2001
S.Speci
                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-225 < RRA>
A;Cross-references: GB:S52569
B;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
B;Ayres, M.D.; Howard, S.C.; Muzio, J.; Lopez-Ferber, M.; Possee, R.D.
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Accession: H72851
A;Cross-references: GB:L22888; NID:9510708; PIDN:AAA66646.1; PID:9559085
C;Comment: The gene is located in a 3-kilobase Xbal genome fragment.
C;Genetics:
C;Genetics:
genomic organization of the EcoRI-A fragment of Autographa californid
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C;Superfamily: Autographa californica nuclear polyhedrosis virus DA26 protein
C;Keywords: early protein
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A;Molecule type: DNA
A;Residues: 1-226 <WIL>
A;Cross-references: EMBL;Z70211; PIDN:CAA94158.1; GSPDB:GN00028; CESP:K11E4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 Accession: T23611
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                                                                       A;Reference number: A44221; MUID:93079853; PMID:1333113
A;Accession: A44221
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50.0%; Pred. No. 5.3e+02;
tive 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 25; DB 1;
Pred. No. 5.3e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, March 1996
A;Reference number: 219770
A;Accession: T23611
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Caenorhabditis elegans
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T2361
hypothetical protein K11E4.2 -
C;Species: Caenorhabditis elega
C;Date: 15-Oct-1999 #sequence_r
C;Accession: T23611
R;Gajadsty, S.
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195 FEFINPDE 202
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GEFIIRDS 177
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Best Local Similarity
Matches 4; Conserv
A; Title: Sequence,
                                         VP8 of rotavirus.
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C;Species: Pyrococcus abysis:
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: C75210
C;Accession: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struch; A;Accession: C75210
A;Accession: C75210
A;Accession: C75210
A;Accession: Draininary
A;Accession: Draininary
A;Residues: 1-27 < KAWA
A;Residues: 1-27 < KAWA
A;Residues: 1-27 < KAWA
A;Coss-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49130.1; PID:g545763
C;Genetics:
A;Genetics:
A;Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein PH0226 - Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: C71248
M;Ohluku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Hino, Y.; Yamazaki, J.; Rushida, N.; Oguchi
DNA Res.; 5-6, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: C71246
A;Accessi
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A)Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29298.1; PID:g3256615
A)Experimental source: strain OT3
A)Experimental source: strain OT3
A)Note: this accession replaces an interim accession for a sequence replaced by GenBank
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GenCore version 5.1. Copyright (c) 1993 - 2004 Comp	protein search, using sw model	September 11, 2004, 21:30:41 ; Se (with 9.467	US-09-660-302E-1 25 1 XEFIXXDX 8	BLOSUM62DX Gapop 10.0 , Gapext 0.5	141681 seqs, 52070155 residues	hits satisfying chosen parameters	.ength: 0 .ength: 200000000	Minimum Match 0% Maximum Match 100% Listing first 300 summaries	ot 42:*	- ber of results r equal to the	SUMS	4	Length DB ID	100.0 54 1 YOLK BPT4 100.0 91 1 VES HPV13 100.0 06 1 MCDE TITMAN	1001	118 1	146 1 STM2	165 1	172 1	175	190 1	192 1	1961	201 1	206	209	213 1	217 1 219 1	225 1 226 1	227 1 ORN A 228 1 BIOW
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                                                    MEDLINE=22514363; PubMed=12626685;
Miller B.S., Kutter B., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
"Bacteriophage T4 genome.";
Microbiol. Mol. Biol. Rev. 67:86-156(2003).
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54 AA; 5897 MW; 972C516A70FE8609 CRC64;
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4; Mismatches
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Pfam; PF05776; Papilloma_E5A; 1.
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Hypothetical protein.
CONFLICT 26 1
   Virol. 67:2305-2316(1993)
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                                                                                                                                                                                              OVIB
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
                                                                                                     Q9zmj6
P56124
Q42694
Q28172
Q28235
Q46561
                                                                                                                                                                                                         P40439
P53051
P32132
O14772
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P38700
P55296
Q9exn7
Q02092
Q90375
Q83120
P42555
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QBrfs6
Q58138
Q8di39
P73580
Q8yti9
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Q28575
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P10912
P79194
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P16310
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93228; Q9TOVB;
01-FBB-1995 (Rel. 31, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
Hypothetical (Rel. 42, Last annotation update)
Hypothetical 5.9 kDa protein in Gp58-sp intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                   SYP_HAEIN
SYP_HELPJ
SYP_HELPY
RUBA_CHIRE
PRLR_BOVIN
                                                                                                                                                                                                                                                                           GLMS_PYRFU
LEPA_CHLMU
LEPA_CHLTR
YHO2_YEAST
APM2_YEAST
MANA_PIRSP
TYPA_ECOL6
GHR_COLLI
LEPA_ENTFA
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GHR SHEEP
MERH DROME
COOS METKA
GHR HUMAN
NPRE_BACCE
MANC_PIRSP
YL53_YEAST
MANB_PIRSP
SYP_BUCAP
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MAZS_YEAST
TYPA_ECOLI
FPGT_HUMAN
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TYPA_HAEIN
SYP_SYNY3
SYT_FUSNN
COOS_METJA
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UVRC_SYNY3
UVRC_ANASP
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NCBI_TaxID=10665;
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-92391075; PubMed=1325697;
van Ranst M., Fuse A., Fiten P., Beuken B., Pfister H., Burk R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: comparison of the genome organizations."; Virology 190:587-596(1992).
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                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
91 AA
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Genew; HGNC:7051; SCGB2A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Tears;
MEDLINE=98163342; PubMed=9504814;
Molloy, M.P., Bolis S., Herbert B.R., Ou K., Tyler M.I., van Dyk D.D.,
Willcox M.D., Gooley A.A., Williams K.L., Morris C.A., Walsh B.J.;
"Establishment of the human reflex tear two-dimensional polyacrylamide
gel electrophoresis reference map: new proteins of potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Lipophilin, a novel heterodimeric protein of human tears.";
FEBS Lett. 432:163-167(1998)
-!- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS, MAY ALSO BIND
-:- FUNCTION: A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER.
MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.
-!- SUBMULT: HETERODIMER OF A LIPOPHILIN A AND A LIPOPHILIN C
-!- TISSUE SPECIFICITY: Expressed in thymus, trachea, kidney, steroid responsive tissues (prostate, testis, uterus, breast and ovary)
                                                                                                                                       30-MXY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
Mammaglobin B precursor (Mammaglobin 2) (Lipophilin C) (Lacryglobin)
(Secretoglobin family 2A member 1).
SCGB2A1 OR MGB2 OR UGB3 OR LIPHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and salivary gland.
MASS SPECTROMETRY: MW=8854.94; METHOD=Electrospray; RANGE=19-95.
SIMILARITY: Belongs to the uteroglobin family. Lipophilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98385871; PubMed=9720917;
Lebrer R.I., Xu G., Abduragimov A., Dinh N.N., Qu X.-D., Martin D.,
Glasgow B.J.;
                                                                                                                                                                                                                                                                                                                                                   "Identification of mammaglobin B, a novel member of the uteroglobin
                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99026127; PubMed=9806831;
Becker R.M., Darrow C., Zimonjic D.B., Popescu N.C., Watson M.A.
Fleming T.P.;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=99167354; PubMed=10066439;
Zhao C., Mguyen T., Yusifov T., Glasgow B.J., Lehrer R.I.;
"Lipophilins: human peptides homologous to rat prostatein.";
Biochem. Biophys. Res. Commun. 256:147-155(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 19-46 AND 60-78, AND MASS SPECTROMETRY
                                                                                                    95 AA
                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ectrophoresis 18:2811-2815(1997)
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                                                                                                                                30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                       gene family.";
Genomics 54:70-78(1998).
                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic value.",
               : | | | :: | :
1 MEFIPVDV
1 XEFIXXDX
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                                                                                                    MGBB HUMAN
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MEDINE=91045079; PubMed=2235495;
TAYLOR M.T.M., Dunt A.A., Coutts R.H.A.;
"Conservation of the 3' terminal nucleotide sequence in five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSCRIPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Length 101;
                                                                                                                                                                                                                                                                                                                  DB 1; Length 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-ARR-1993 (Rel. 25, Last annotation update)
11.6 kDa protein (Putative nucleic acid-binding protein).
                                                                                                                                                                                                                                                                                                                                                            0; Indels
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SBDF36C3A14A5091 CRC64;
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                                       InterPro; IPR003627; Mamgb/prostatn.
InterPro; IPR000329; Uteroglobin_subf.
InterPro; IPR0006038; Uteroglobin_supf.
Pfam; PF01099; Uteroglobin; 1.
ProDom; PD029354; Mamgb/prostatn; 1.
PROSTIE; PS00403; UTERGGLOBIN_1; FALSE NEG.
PROSTIE; PS00404; UTEROGLOBIN_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                      Pred. No. 94;
4; Mismatches
                                                                                                                                                                                                                                 MAMMAGLOBIN B
                                                                                                                                                                                                                                                                                                                  Score 25;
MIM; 604398; -.
GO; GO:0005497; F:androgen binding; NAS.
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InterProc, Impro02568, Carla_C4.
Pfam, PF01623, Carla_C4; 1.
Zinc-finger; DNA-binding.
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                                                                                                                                                                                                                                                                         95 AA; 10884 MW;
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                                                                                                                                                                                          Signal; Glycoprotein.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLV
                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
VNBP_CLV
ID VNBP (
                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                          Matches
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=12950922;
Zhang Y.-C., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.,

"Genome-based analysis of virulence genes in a non-biofilm-forming
Staphylococcus epidermidis strain (ATCC 12228).",

Mol. Microbiol. 49:1577-1593(2003).

-! FUNCTION: Involved in the transcription termination process (By
                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·.
                                                                                                                                                    Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Nutilization substance protein B homolog (NusB protein).
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 1; Length 12
50.0%; Pred. No. 1.38+02;
ive 4; Mismatches 0; Indels
                                                            .l protein.
118 AA; 13412 MW; 3FEBF7A48658E208 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription termination, Complete proteome.
SEQUENCE 129 AA; 15150 MW; 161923DD8535AlCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Firmicutes, Bacillales, Staphylococcus
                                                                                                                                              100.0%; Score 25; DB 1; 50.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STW2 MOUSE STANDARD; PRT; 146 AA. P83093; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Stromal interaction molecule 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-!- SIMILARITY: Belongs to the nusB family.
                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
EMBL; K01263; -; NOT_ANNOTATED_CDS.
PIR; A03800; QQBE8H.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE016748; AA004804.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF 00073; -; 1.
InterPro; IPR006027; NusB.
Pfam; PF01029; NusB; 1.
                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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28 OEFITNDV 35
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30 IEFIKDDH 37
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                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=ATCC 12228;
                                                                                                                                                                                                                                                                 1 XEFIXXDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUSB OR SE1205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUSB STAEP
                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUSB_STAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STM2_MOUSE
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
   S K B B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                               Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 25; DB 1; Length 109; Pred. No. 1.1e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 AA; 12053 MW; 597E7F7137389454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2010 (Rel. 40, Last annotation update)
Hypothetical 13 kDa protein in transforming region.
                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ECORI-T site protein ETM homolog.
                                                                                                                109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                         Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|||::|:
96 LEFIKLDV 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Early protein.
                                                                        VETM_NPVOP
ID VETM_NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y13K HCMVA
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                                                                                                                                     010307;
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Y13K HGWVA
IN 13K HGWVA
AC P03236,0
DT 21-JUJL.
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DE BETANE.
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47 PEFIILDM
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                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
                                                                                                                                                     proteins.;
Biochem. J. 357:673-688 (2001)

-!- FUNCTION: Possible adhesion molecule with a role in early hematopoiesis by mediating attachment to stromal cells. Influences the survival and/or proliferation of B cell precursors. Binding to cells requires Mn(II) (By similarity).
-!- SUBGNIT: Oligomer with STIM1 (By similarity).
-!- SUBCELIULAR LOCATION: Type I membrane protein. Cell surface
                                                                  STRAIN=C57BL/6J; TISSUB=Skeletal muscle;
MEDLINE=21356314; PubMed=11463338;
Williams R.T., Manji S.S.M., Parker N.J., Hancock M.S.,
Wan Stekelenburg L., Bid J.-P., Senior P.V., Kazenwadel J.S.,
Shandala T., Saint R., Smith P.J., Dziadek M.A.;
"Identification and characterization of the STIM (stromal interaction molecule) gene family: coding for a novel class of transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97305956; PubMed-9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
Perret X.;
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                    (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobium/Agrobacterium group, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 25; DB 1; Lengu...; No. 1.5e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SWART; SM00454; SAM; 1.
PROSITE; PS50105; SAM DOMAIN; 1.
Cell adhesion; Transmembrane; Coiled coil; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 AA; 17321 MW; 503740533EEB0F63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 17.3 kDa protein Y4JR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:2151156; Stim2.
GO; GO:0005515; F:proctein binding; IPI.
InterPro; IPR001660; SAM.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAM.
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF328907; AAK82339.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 DEFIREDM 19
 musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                            SEQUENCE FROM N.A.
                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
55
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-:- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin = protein L-methionine S-oxide + reduced thioredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EC 1.8.4.6) (Protein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Е.Ү.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
VCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
"Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 1; Length 151; 50.0%; Pred. No. 1.6e+02; tive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen
Cassell G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Peptide methionine sulfoxide reductase msrA (EC 1.8.4.6)
methionine-S-oxide reductase) (Peptide Met(O) reductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 151 AA; 17262 MW; F8B42BCF7845E03F CRC64;
                             Nature 387:394-401(1997).
-!- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50110; RESPONSE REGULATORY; 1. Hypothetical protein; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Serovar 3;
MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000080; AAB91730.1; -.
BTR; T28645; T28645.
InterPro; IPR001789; Response_reg.
SWART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE002125; AAF30698.1; -.
HSSP; P54149; 1FVG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAE, MF 01401; -; 1.
InterPro; IPR002569; PMSR.
Pfam; PF01625; PMSR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            urealyticum.";
Nature 407:757-762(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
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ALL1 RHIME

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Gamma-N-methylasparagine in phycobiliproteins. Occurrence, location,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 236:167-170(1988).
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=85063716; PubMed=6438628;
Pilot T.J., Fox J.L.;
"Cloning and sequencing of the genes encoding the alpha and beta
subunits of C-phycocyanin from the cyanobacterium Agmenellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duerring M., Huber R., Bode W., "The structure of gamma-N-methylasparagine in C-phycocyanin from Mastigocladus laminosus and Agmenellum quadruplicatum.",
                                                                                                                      Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGR01339; phycocy beta; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                          de Lorimier R., Bryant D.A., Porter R.D., Liu W.-Y., Jay E., Stevens S.B. Jr., "Genes for the alpha and beta subunits of phycocyanin."; Proc. Natl. Acad. Sci. U.S.A. 81:7946-7950(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from the phycobiliprotein complex.
-!- SUBUNIT: Heterodimer of an alpha and a beta chain.
-!- PTM: Contains two covalently linked bilin chromophores.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHYCOCYANOBILIN CHROMOPHORE. PHYCOCYANOBILIN CHROMOPHORE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quadruplicatum.";
Proc. Natl. Acad. Sci. U.S.A. 81:6983-6987(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 1; Le
50.0%; Pred. No. 1.8e+02;
tive 4; Mismatches 0;
             23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TERTIARY STRUCTURE AROUND METHYLATED SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 262:17350-17355(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, P07119; 1CPC.
InterPro; IPR001659; Phycobilisome
InterPro; IPR006247; Phycocyanin b.
Pfam; PF00502; Phycobilisome; I.
ProDom; PD000340; Phycobilisome; I.
                                                                                                                                                                                                                                                    MEDLINE=85088525; PubMed=6096868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88087010; PubMed=2447072;
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82 82 PH)
153 153 PH)
172 AA; 18336 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; K02660; AAB05343.1; -. EMBL; K02659; AAB05341.1; -.
                                                                              2-phycocyanin beta chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klotz A.V., Glazer A.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 50.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                               NCBI_TaxID=32049;
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                                                                                                                                                                                                                                    STRAIN=PR-6;
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Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
Golding B., Puehler A.,
Finan Googlete sequence of the 1.683-kb pSymB megaplasmid from the N2-
fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
-!- CATALYITC ACTIVITY: (-)-ureidoglycolate + H(2)O = glyoxylate + 2
NH(3) + CO(2).
-!- PATHWAY: Degradation of allantoin (purine catabolism); third step.
-!- SIMILARITY: Belongs to the ureidoglycolate hydrolase family.
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Froteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                        Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; Length 170; 50.0%; Pred. No. 1.8e+02; ive 4; Mismatches 0; Indels
                                                                                                                                  100.0%; Score 25; DB 1; Length 16
50.0%; Pred. No. 1.7e+02;
Live 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF 00616; -; 1.
InterPro; IPR00747; Ureidogly_hydro.
InterPro; IPR00747; Ureidogly_hydro.
HydroLase; Purine metabolism; Plasmid; Complete proteome.
SEQUENCE 170 Aa; 18930 MW; 051CACE71CEF9CDF CRC64;
                                                                                         678DC470BBE22AAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
20-FEB-2003 (Rel. 41, Last annotation update)
ALLAI OR RELIGT OR SME20873.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                               170 AA
ProDom; PD003489; PMSR; 1.
TIGREAMS; TIGR00401; msrA; 1.
Oxidoreductase; Complete proteome.
ACT_SITE 11 11 BY SIMILARITY.
SEQÜENCE 165 AA; 19341 MW; 678DC470BBEZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL603646; CAC49567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pSymB (megaplasmid 2)
                                                                                                                                                   Local Similarity 50.0
les 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                  : | | | :: |:
105 DEFIIKDF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 SEFIVVDR 143
                                                                                                                                                                                                                       1 XEFIXXDX 8
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                                                                                                                                  Query Match
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Q92UG4;
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172 AA.

PRT;

STANDARD;

Matches

Length 172;

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                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Mol. Biol. Rep. 13:336-342(1995).

-!- FUNCTION: Probably participates in efficiency of electron transfer from plastocyanin to P700 (or cytochrome c533 in algae and cyanobacteria). This plastocyanin-docking protein contributes to the specific association of plastocyanin to PSI.

-!- SUBCELLUIAR LOCATION: Associated with lumenal side of the
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-22514363; PubMed=12626685;
Miller E.S., Kutter E., Mosig G., Arisaka.F., Kunisawa T., Ruger W.;
                                                                                                                                                                                                                   genes tk and nrdC: twenty new t4 genes, generally conserved among T-even phages."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                          Mzhavia N., Marusich E., Djavakhishvili T., Neitzel J., Peterson Awaya M., Eidermiller J., Canada D., Tracy J., Gailbreath K., Paddison P., Anderson B., Stidham T., Blattner F., Kutter E.M.; "The 10.7 kb 'nonessential' region of bacteriophage T4 between th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast.
Eukaryota, stramenopiles, Bacillariophyta, Coscinodiscophyceae,
            no RNA stage; Caudovirales; Myoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freit
"The chloroplast genome of a chlorophyll a+c-containing alga,
Odontella sinensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 25; DB 1; Length 17
Pred. No. 1.9e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 175 AA; 20757 MW; 12ABE25E9AEC5219 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Photosystem I reaction centre subunit III (PSI-F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the psaF family.
                                                                                                                                                                                                                                                                                                                                                                                         "Bacteriophage T4 genome.";
Microbiol. Mol. Biol. Rev. 67:86-156(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Odontella sinensis (Marine centric diatom)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF158101; AAD42639.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
50.0%; I
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Best Local Similarity 50.v.
4, Conservative
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                Viruses; dsDNA viruses,
T4-like viruses.
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                                                                                                         SEQUENCE FROM N.A.
                                                              NCBI_TaxID=10665;
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Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Heidelberg J.F., Eisen J.A., Nelson W.C., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 406,477-483(2000).
-!- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01128; SHIKIMATE KINASE; 1.
Aromatic amino acid biosynthesis; Transferase; Kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19:3925; 096220; 01-FEB-1995 (Rel. 31, Created) 15-7010-1998 (Rel. 36, Last sequence update) 10-007-2003 (Rel. 42, Last annotation update) 10-007-2003 (Rel. 42, Last annotation update) 10-007-2003 (Rel. 92) Paper annotation update) 10-007 NDD NRDC.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 1; Length 174; 50.0%; Pred. No. 1.8e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the shikimate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IP (BY SIMILARITY).
206FABCBFA9981CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fifth step.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable)
                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 AA
                                                                                                                                           10-OCT-2003 (Rel. 42, Last annotation
Shikimate Kinase (BC 2.7.1.71) (SK).
AROK OR VC2629.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=El Tor N16961 / Serotype O1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP, MF 00109; -; 1.
InterPro, IPR000623; Shik kinase.
Pfam; PF01202; SKI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004329; AAF95770.1; -.
HSSP; P10880; 1SHK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01100; SHIKIMTKNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19618 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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30 MEFIDSDT
                                                                                                                                                                                                                               Vibrio cholerae
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=666;
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                                                                                                                0-0CT-2003
                                                                                                                                    10-OCT-2003
                                                                     AROK VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholerae.
                                                                                      OPKNV1;
                        RESULT 13
AROK_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Gaps

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185 AA

Length 175;

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GLPP_BACSU
P30300;
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   CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                      SEQUENCE
                                                                                                       Query Match
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                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                         RESULT 17
       FFF
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              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC 35210 / B31;
STRAIN-ATCC 35210 / B31;
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; Pubm6d=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavarde A., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer W., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.,
"Genomic sequence of a Lyme disease spirochaete, Borrelia
       п
                                                                                                                                                                                                                                         Gaps
       ŗ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Telomeres of the linear chromosomes of Lyme disease spirochaetes: nucleotide sequence and possible exchange with linear plasmid
                                                                                                              InterPro; IPR003666; PSI_PsaF.
Pfam; PF02507; PSI_PsaF; 1.
Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.
SEQUENCE 185 AA; 20747 MW; 16C70038FAD4F048 CRC64;
                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                    DB 1; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Casjens S., Murphy M., Delange M., Sampson L., van Vugt R.,
       as its content
                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> M (IN REF. 2)
                                                                                                                                                                                                  100.0%; Score 25; DB 1;
50.0%; Pred. No. 2e+02;
ive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                                                                                                                                                                                    Y001_BORBU STANDARD; PRT; 190 AA. 051035; 051894; 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Complete proteome CONFLICT 12 I -> M (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sh-2-82;
MEDLINE=98065594; PubMed=9402027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Microbiol. 26:581-596(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE001115; AAC66406.1; -. EMBL; AF008218; AAB93996.1; -.
                                                                                EMBL; Z67753; CAA91702.1; -. PIR; S78329; S78329.
                                                                                                                                                                               Query Match
Best Local Similarity 50.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein BB0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390:580~586(1997).
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QEFISNDL 173
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TIGR; BB0001; -.
                                                                                                                                                                                                                                                                       1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
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Y001_BORBU
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brigarell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Cadani J.J., Pusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Rabert C., Ferrari E., Foulger D.,
RA Ghim S.Y., Calser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Koaramata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koninosstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Mallado R.P., Mizuno G., Rodiga B., Roseson M.,
Rain Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Ranto V., Scanlan E., Schleich B., Rapoport G., Perscott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rateger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
Rateger M., Rivolta C., Roche B., Rose M., Sadaie Y.,
Rateger M., Tamakoshi A., Tarakanashi H., Takamaru K.,
RA Sorokin A., Tarakai T., Terpstra P., Tognoni A.,
Rakeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the glyB marker, many genes encoding transporter proteins, and the ubinitons hir neem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R., Wedler H., Venema G., Bron S., "The 172 kb prkA-addB region from 83 degrees to 97 degrees of Bacillus subtilis chromosome contains several dysfunctional gen
                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beijer L., Nilsson R.-P., Holmberg C., Rutberg L.; "The glpp and glpF genes of the glycerol regulon in Bacillus subtilis.";
                                                                                                          Score 25; DB 1; Length 190; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                  (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 42, Last annotation update)
:ake operon antiterminator regulatory protein.
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                       FBFCE799CD827B45 CRC64;
 6
               KI -> NL (IN REF. 2).
S -> P (IN REF. 2).
S -> I (IN REF. 2).
                                                                                                                                               ;
 EDL -> GDI (IN REF.
                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gen. Microbiol. 139:349-359(1993).
                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=93171878; Pubmed=8436953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98240224; PubMed=9579061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microbiology 144:859-875(1998)
                                                                       22491 MW;
                                                                                                          100.08;
                                                                                                                           50.0%;
                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                 STANDARD;
 36
41
81
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177 KEFILLDL 184
                                                                                                                                                                                    1 XEFIXXDX 8
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                                                                       190 AA;
                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                            GLPP OR BSU09270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1423;
34
40
53
81
                                                                                                                                                                                                                                                                                                                                                                                                              Glycerol uptake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ubiquitous hit
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ECOLI
                                                                                                                                                                         YG5C_YEAST
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                                                                                                                                                                                        P53317;
                                                                                                                                              RESULT 19
YGSC YEAST
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                                           Matches
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                     Nature 390:249-256(1997).
-!- FUNCTION: IN THE PRESENCE OF GLYCEROL 3-PHOSPHATE, THIS PROTEIN IS THOUGHT TO ENHANCE PRANSCRIPTION.
-!- SIMILARITY: TO E.COLI YGCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä
                                                                                                                                                                                                                                                                                     EMBL; 299108; CAA74427.1; -.
EMBL; Z99108; CAB12755.1; -.
EMBL; Z99108; CAB12755.1; -.
Subtilist; BG10185; 91pP.
InterPro; IPR003009; FMN enzyme.
InterPro; IPR006699; G3P antiterm.
Pfam; PP04309; G3P antiterm.
Olycerol metabolism; Transcription regulation; Complete proteome.
SEQUENCE 192 AA; 21609 MW; E3B9A85C5AFA3949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97305956; PubMed-9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal .
Perret X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
-!- SIMILARITY: None obvious.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid sym_pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 1; Length 192; 50.0%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AE000070; AAB92444.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 192 AA; 20638 MW; A2B0B751AD579EB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 20.6 kDa protein Y4DX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.1e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                            EMBL; M99611; AAA22489.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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71 AEFICQDI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y4DX RHISN
P55423;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 18
Y4DX_RHISN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                       Gaps
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Analysis of a 17.9 kb region from Saccharomyces cerevisiae chromosome VII reveals the presence of eight open reading frames, including BRF1 (TFIIIB70) and GCNS genes."; Yeast 13:373-377(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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Feroli F., Carignani G., Pavanello A., Guerreiro P., Azevedo I
Rodrigues-Pousada C., Melchioretto P., Panzeri L.,
Agostoni Carbone M.L.;
                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last amoutation update)
Hypothetical 22.3 kDa protein in MGA1-GCN4 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 196;
100.0%; Score 25; DB 1; Length 192; 50.0%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2320 Mw; ...
100.0%; Score 25; DB 1; Lenguu -.
red. No. 2.1e+02;
0; Indels
                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 AA; 22320 MW; 9D106ADCA2BF018E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-2001 (Rel. 40, Last annotation update)
Hypothetical protein ykgK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 AA.
                                                                                                                                                                                                                                                                                           196 AA
                           50.0%; Pred. No. 2.1e ive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z73036; CAA97280.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                       4; Conservative
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                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|||::|:
93 GEFIEGDK 100
                                                                                                                                                            118 VEFIEDDP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S64583; S64583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 XEFIXXDX 8
                                                                                                           1 XEFIXXDX 8
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     Query Match
Best Local Similarity
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204 AA.
                    SIMILARITY: Belongs to the IF-3 family.
                                                                                                                                                                                                                                                                                         entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22538493; PubMed=12538648;
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                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AE000004, AAG34732.1; -. PIR; S73365; S73365. HSSP, PO3000, ITTF. HAMP, MF 00080; -1. InterPro; IPR001288; IF3. Pfam; PF00707; IF3. C. Ir Pfam; PF05198; IF3. N. ProDom; PD002880; IF3. N. ProDom; PTGREAMS; TICRO168; InfC; I. TICRFAMS; TICRO168; InfC; I. Promission of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
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44 NEFILIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2190;
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Matches
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DCD_METJA
                    SO WE WE WE WE WAS A SECOND COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR CO
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Nucleic Acids Res. 24:4420-4449(1996).

-!- FUNCION: IF-3 binds to the 30S ribosomal subunit and shifts the equilibrum between 70S ribosomes and their 50S and 30S subunits in favor of the free subunits, thus enhancing the availability of 30S subunits on which protein synthesis initiation begins.
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                        STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattine F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maynew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis Dederspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Swamath A., Oefner P., Roberts D., Schramm S., Davis R.W., Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 25; DB 1; Length 196; Pred. No. 2.1e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodom; PD000307; HTH LuxR; 1.
SWART; SM00421; HTH LUXR; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 196 AA; 23274 MW; 5A3676E17E9793B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 AA
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MEDLINE=97105885; PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000137; AAC73397.1; -. PIR; F64755; F64755. EcoGene; EG14324; ykgK. InterPro; IPR000792; HTH_LuxR. Pfam; PF00196; GerE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                 Gregor J., Dav.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
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P78024;
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Matches

RESULT 21

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SEQUENCE FROM N.A.
SINGUEDE TO N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; Pubmed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Tomb J.P., Adams M.D.,
Karlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,
Stoctt J.L., Geoghagen N.S.M., Weidman J.E., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kallay J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Bifunctional deaminase/diphosphatase (MjDCD-DUT) (DCD/DUT) [Includes: Deoxycytidine triphosphate deaminase (BC 3.5.4.13) (dCTP deaminase);
Deoxyvridine 5'-triphosphate nucleotidohydrolase (BC 3.6.1.23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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"The Methanococcus jannaschii dCTP deaminase is a bifunctional
deaminase and diphosphatase.",
"Biol. Chem. 278:11100-11106 (2003).
-!- FUNCTION: Catalyzes two consecutive reactions to form dUMP using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION, MASS SPECTROMETRY, AND MUTAGENESIS OF ASP-135 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initiation factor; Protein biosynthesis; Complete proteome.
SEQUENCE 201 AA; 23145 MW; 3E14B9FA797C80C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25, DB 1; Lv
Pred. No. 2.2e+02;
4; Mismatches 0;
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InterPro; IPR002136; Ribosomal_L4/L1E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Madrid E; MEDLINE=99039393;
                                                                                                                                                                                                                                                       RL4 RICPR STANDARD; E Q9ZCG6; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequin-coll-2001 (Rel. 40, Last annotation)
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                                                                                                                      50.0%;
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Best Local Similarity 50...
4; Conservative
                                                                                                                                     4; Conservative
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                                                                                                                                                                                                                                                                                                                                                       Rickettsia prowazekii.
                                                                                                                                                                                        134 PEFIEVDV 141
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                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitochondria."
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P39149;
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                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                     Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gryaznova O.I., Davydova N.L., Gongadze G.M., Jonsson B.-H.,
Garber M.B., Liljas A.;
A ribosomal protein from Thermus thermophilus is homologous to a
general shock protein ",
Biochimie 78:915-919(1996).
--- FUNCTION: BINDS TO THE 58 RRNA.
--- SIMILARITY: Belongs to the L25P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                       -i- ENZYME REGULATION: Inhibited by dTTP.
-i- PATHWAY: De novo synthesis of thymidylate.
-i- SUBUNIT: Homohexamer (Probable).
-i- MASS SPECTROMETRY: MW=23619; MW ERR=94; METHOD=MALDI.
-i- MASS SPECTROMETRY: MW=23619; MW ERR=94; METHOD=MALDI.
-i- MISCELLANBOUGS: Optimal pH is 7.5. Retained over 70% of its activity when heated at 90 degrees Celsius for 10 min.
-i- SIMILARITY: Belongs to the dCTP deaminase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 1; Length 204; 50.0%; Pred. No. 2.2e+02; ative 4; Mismatches 0; Indels
CATALYTIC ACTIVITY: dCTP + H(2)O = dUTP + NH(3).
CATALYTIC ACTIVITY: dUTP + H(2)O = dUMP + diphosphate.
COFACTOR: Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 50S ribosomal protein L25 (TL5).
Thermus thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=VK1;
MEDLINE=97295226; PubMed=9150868;
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30-MAY-2000 (Rel. 39, Last sequ
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                          EMBL; U67494; AAB98415.1; -. PIR; F64353; F64353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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DEFIIYDD 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=274;
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P56930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the L4P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=782;
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50.0%; Pred. No. 2.2e+02;
.ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                       0; Indels
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Ribosomal protein; rRNA-binding; Complete proteome.
SEQUENCE 207 AA; 23288 MW; AA652123EB22797E CRC64;
                                                                                                                                                        E6C214CAF141316C CRC64;
                                                                                                                                                                                                            100.0%; Score 25; DB 1;
50.0%; Pred. No. 2.2e+02;
ive 4; Mismatches 0
EMBL, X94435; CAA64209.1; -.
PDB; 1FEU; 25-JUN-01.
InterPro; IPR001021; Ribosomal L25.
TIGRRAMS; TIGR00731; ctc TL5; ī.
TIGRRAMS; TIGROFF, RNA-binding; 3D-structure.
SEQUENCE 206 AA; 23218 MW; E6C214CAF141316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 39, Last sequence update)
50S ribosomal protein L4.
Rible OR RP658.
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Length 209;

(UPRTase)

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Pfam; PF00156; Pribosyltran; 1.
TIGRPAMs; TIGR01091; upp; 1.
Transferase; Glycosyltransferase; Magnesium; Complete proteome.
DOMAIN 127 139 PRPP-BINDING (BY SIMILARITY).
DOMAIN 193 201 UMP-BINDING, URACIL PART (BY SIMILARITY).
                                                                                                                                                                                                   457C6810A3651564 CRC64;
                                                                                                                                                                                                   209 AA; 23037 MW;
                                                                                                                                                                                                                                                            100.0%;
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125 REFIVVDP 132
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                               SEQUENCE
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                            SO FT SO
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Ry Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., Rubrills."

Rubrils."
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                                                                                 (UMP pyrophosphorylase)
                                                                                                                                                                                                                                                                                                                                                                                                                 Martinussen J., Glaser P., Andersen P.S., Saxild H.H.;
"Two genes encoding uracil phosphoribosyltransferase are present in
Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: UMP + diphosphate = uracil + 5-phospho-
alpha-D-ribose 1-diphosphate.
COFACTOR: Magnesium (By similarity).
                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: Pyrimidine salvage pathway.
-!- SIMILARITY: Belongs to the UPRTase family.
01-FEB-1995 (Rel. 31, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Uracil phosphoribosyltransferase (EC 2.4.2.9)
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HSSP, 026998; 1BD3.
Subtilist; BG10945; upp.
HAMAP: MF 01218; -; 1.
InterPro; IPR000836; PRTransferase.
InterPro; IPR005765; Ura_phspho_trans.
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95095982; PubMed=7798145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 177:271-274(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z38002; CAA86111.1; -. EMBL; Z99122; CAB15706.1; -.
                                                                                                                                          UPP OR IPC-35D OR BSU36890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: Magnesium
                                                                                                                                                                      Bacillus subtilis.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                 STRAIN=168
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A Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Ra Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Ragouros U., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros U., Barker S., Basham D., Bowman S., R. Brown D., Brown S., Chillingworth T., Churcher C.M., A. Collins M., Connor R., Taris D., Hidalgo J., Hodgson G., R. Hamlin M., Harris D., Hidalgo J., Hodgson G., R. Holroyd S., Hornsby T., Howarth S., Huchle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., R. Monney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., R. Oliver K., O'Neil S., Rauders D., Seeger K., Sharp S., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Taylor K., Taylor K., Gwill S., Rab S., Stevens K., Taylor K., Taylor K., Robben J., Gymonptez B., Rabelton J., Volckaert G., Aert R., Robben J., Gymonptez B., Weltjens I., Vanstreels E., Reger M., Schaefer M., Mueller-Auer S., Rabelton J., Stumermann W., Wedler H., Wambutt R., Purnelle B., Rabelt C., Fuchs M., Wedler H., Wambutt R., Purnelle B., Radelber J., Sanchez M., Galibert F., Aves S.J., Xiang Z., Hunt C., More K., Hurst S., M., Baga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benitto J., Abaga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benitto J., Abaga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benitto J., R. Dominguez A., Revurelta J.L., Moreno S., Ammerrong J., Forburg J., Proben R.R., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., Haripe A., Revire 415-RPI.
                                                  Gaps

    -!- FUNCTION: Catalyzes the conversion of dTMP to dTDP.
    -!- CATALYTIC ACTIVITY: ATP + thymidine 5'-phosphate = ADP + thymidine

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abaigar L.T., Yeh Y.I., Jong A.Y., "Functional and structural conservation of Schizosaccharomyces pombe dTMP kinase gene.";
                                                     .
100.0%; Score 25; DB 1; Length 20
50.0%; Pred. No. 2.38+02;
ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5'-diphosphate.
-!- PATHWAY: Blosynthesis of dTTP from dTMP.
-!- SIMILARITY: Belongs to the thymidylate Kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)
TMP OR SPCC70.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1132:222-224(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21848401; PubMed=11859360;
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EMBL; L33462; AAC41483.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                  DIR; $28955; $28955.
PIR; 741553; T41553.
HSSP; P00572; JTMK.
GeneDB SPombe; SPC70:07c; -.
InterPro; IPR000062; Thymidylate kin; InterPro; IPR00062; Thymidylate kin; I.
Pfam; PP02223; Thymidylate kin; I.
PROSITE; PS01331; THYMIDYLATE KINASE; I.
PROSITE; PS01331; THYMIDYLATE KINASE; I.
Transferase; Kinase; Nucleotide biosynthesis; ATP-binding.
NP BIND
OWNFILCT 33 39 SQBEKAE -> INMICH.
CONFLICT 59 59 K -> T (IN REF. 1).
CONFLICT 69 93 TIQYINGUT -> PSIYYRANQQRCN (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutant of Helicobacter mustelae.";
Infect. Immun. 63:3718-3721(1995).
-!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-!- SUBUNIT: CONSIST OF TWO SUBUNITS (ALPHA AND BETA).
-!- CAUTION: IN HELICOBACTER THE ALPHA SUBUNIT IS WHAT IS KNOWN, IN OTHER BACTERIA AS THE BETA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=NCTC 12032;
BEDLINE=95369940; PubMed=7642313;
Solnick J.V., Josenhans C., Tompkins L.S., Labigne A.;
"Construction and characterization of an isogenic urease-negative
                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                        Score 25; DB 1; Length 210; red. No. 2.3e+02; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 4266144AEDAB68C0 CRC64;
                                                                                                                                                                                                                                                                                                                           P -> T (IN REF. 1).
F -> L (IN REF. 1).
S -> YA (IN REF. 1).
H -> D (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Pred. No. 2.3e ive 4; Mismatches
                                                                                                                          EMBL; AL023794; CAA19357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 24249 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         100.08;
                                                                                                             EMBL; X65868; CAA46698.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter mustelae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||::|:
LEFITLDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Urease alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                 210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                             125
164
186
191
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                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P50044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            URE1 HELMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 27
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01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable glutathione S-transferase (EC 2.5.1.18) (Pathogenesis-related protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; asterids; lamiids, Solanales, Solanaceae, Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92063197; PubMed=2132026;

Taylor J.L., Fritzeneier K.H., Haeuser I., Kombrink E., Rohwer F., Schroeder M., Strittmatter G., Hahlbrock K.;

Schroeder M., Strittmatter G., Hahlbrock K.;

"Structural analysis and activation by fungal infection of a gene encoding a pathogenesis-related protein in potato.";

Mol. Plant Microbe Interact. 3:72-77(1990).

-! CATALYTIC ACTIVITY: Rx + glutathione = HX + R-S-glutathione.

-! INDUCTION: By fungal infection.

-! SIMILARITY: Belongs to the GST superfamily. HSP26 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 25; DB 1; Length 213;
Pred. No. 2.3e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004046; GST_Cterm.
InterPro; IPR004045; GST_Nterm.
Pfam; PF00043; GST_C; 1.
Pfam; PF02798; GST_N; 1.
Plant defense; Transferase; Pathogenesis-related protein.
SEQUENCE 217 AA; 25056 MW; 7B0DBBE216685B4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 1; Length 21 clarity 50.0%; Pred. No. 2.3e+02; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      1
213 AA; 23794 MW; B97A6A3FD2CB2F40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 AA.
                                                                                                           Interpro; IPR008223; Urease_gammabeta.
Pfam; PF00699; Urease_beta; 1.
Pfam; PF00547; urease_gamma; 1.
PrsSF; PRSF001225; Urease_gammabeta; 1.
ProDom; PD002326; Urease_beta; 1.
ProDom; PD002319; Urease_beta; 1.
                                                                                                                                                                                                                                                                                          TIGRFAMs; TIGR00192; urease_beta; 1.
TIGRFAMs; TIGR00193; urease_gam; 1.
HSSP, P41022; 1UBP.
HAMAP, MF 00739; fused; 1.
InterPro; IPR002019; Urease_beta.
InterPro; IPR002026; Urease_gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J03679; AAA68430.1; -. PIR; T07595; T07595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||::|:
97 GEFILKDE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 XEFIXXDX 8
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                             Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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225 AA

NPVAC

1 XEFIXXDX 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MBDLINE-98049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Karlavage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- CATALYTIC ACTIVITY: ATP + UMP = ADP + UDP.
-!- PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP; first
                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable uridylate kinase (EC 2.7.4.-) (UK) (Uridine monophosphate kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_01220; -; 1.
InterPro; IPR001048; Aa kinase.
Pfam; PF00696; aakinase; 1.
Transferase, Kinase, Pyrimidine biosynthesis; Complete proteome.
SEQUENCE 219 AA; 23398 MW; 751B894ED5261B91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Catalyzes the phosphorylation of UMP to UDP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 1; Length 219; 50.0%; Pred. No. 2.4e+02; ative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaeoglobus fulgidus.
Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the UMP kinase family.
                                                                                                                                                                                                                      219 AA
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaeoglobaceae; Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000962; AAB89213.1; -.
                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:364-370(1997)
:|||::|:
29 YEFIEEDL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A69505; A69505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRH OR AF2042
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                                                                                                                                                                                                           PYRH ARCFU 028237;
                                                                                                                                                                                                           HERE AND THE SECOND COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence, genomic organization of the BcoRI-A fragment of Autographa californica nuclear polyhedrosis virus, and identification of a viral-encoded protein resembling the outer capsid protein VPB of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virology 202:586-605(1994).
-!- FUNCTION: This protein is required for viral late gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90264832; PubWed=2189022; O'Reilly D.R., Passarelli A.L., Goldman I.F., Miller L.K.; O'Reilly D.R., Passarelli A.L., Goldman I.F., Miller L.K.; Characterization of the DA26 gene in a hypervariable region of the Autographa californica nuclear polyhedrosis virus genome."; J. Gen. Virol. 71:1029-1037(1990).
                                                                                                                                                                                                                                                                Guarino L.A., Summers M.D.;
Finctional mapping of Autographa california nuclear polyhedrosis
Fints genes required for late gene expression.";
J. Virol. 62:463-471(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=E2;
MEDLINE=93079853; PubMed=1333113;
Braunagel S.C., Daniel K.D., Reilly L.M., Guarino L.A., Hong T.,
Summers M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C6;
MEDLINE=94303173; PubMed=8030224;
MEDLINE=94303173; PubMed=8030224;
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.,
"The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.";
                                                                                                                             (AcMNPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; Length 22 50.0%; Pred. No. 2.4e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 AA; 25910 MW; D27965D85B2C7980 CRC64;
                                                                                                                     Autographa californica nuclear polyhedrosis virus (A
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                             01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                               MEDLINE=88091055; PubMed=2826808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virology 191:1003-1008(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M22619; AAA69846.1; -.
EMBL; M18857; AAA66808.1; -.
EMBL; M96361; AAA66786.1; -.
EMBL; L22858; AAA6646.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                      Early 25.9 kDa protein.
                                                                                                                                                     Nucleopolyhedrovirus.
NCBI_TaxID=46015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|||::|:
195 FEFINPDE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A29891; WMNV29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 XEFIXXDX 8
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                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rotavirus."
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=L1;
                                                                                                                                                                                                            SEOUENCE
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Gaps

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4; Conservative

Matches

124 AEFIKADV 131

RESULT 30 VE26\_NPVAC

1 XEFIXXDX 8

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eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SEQUENCE
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                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=963-9999; Dubmd=86880887;

Bult C.J., White O., Olsen G.J., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Tomb J.P., Adams M.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: ATP + UMP = ADP + UDP.
-!- PATHWAX: Pyrimidine biosynthesis; conversion of UMP to CTP; first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.74M.Y.2000 (Rel. 39, Created)
30.74M.Y.2000 (Rel. 39, Last sequence update)
16.0CT-2001 (Rel. 40, Last annotation update)
16.0CT-2001 (Rel. 40, Last annotation update)
Probable oligoribonuclease (EC 3.1.-.-).
AT2G26970 OR T20P8.2.
ATAbidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable uridylate kinase (EC 2.7.4.-) (UK) (Uridine monophosphate kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF_01220; -; 1.
InterPro; IPR001048; Aa_kinase.
Pfam; PF00696; aakinase; 1.
Transferase; Kinase; Pyrimidine biosynthesis; Complete proteome.
SEQUENCE 226 AA; 24099 MW; 7052087EE2AE240D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Catalyzes the phosphorylation of UMP to UDP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 1; Length 226; 50.0%; Pred. No. 2.5e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                             Archaea, Euryarchaeota, Methanococci, Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMÎLARITY: Belongs to the UMP kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U67566; AAB99262.1; ALT_INIT.
                                                                 01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                            Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                  Methanococcus jannaschii.
                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 AEFINADL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 XEFIXXDX 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
                                                                                                                                                                                             NCBI_TaxID=2190;
                                                                                                                                    PYRH OR MJ1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MJ1259
                                                                                                                                                                                                                                                                                                                                                                                                jannaschii.
                                  PYRH METJA
Q58656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORN ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9ZVEO;
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                         PYRH_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORN ARATH
        RESULT 31
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10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
6-carboxyhexanoate--CoA ligase (EC 6.2.1.14) (Pimeloyl-CoA synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang Y.-O., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;

"Genome-based analysis of virulence genes in a non-biofilm-forming

Staphylococcus epidermidis strain (ATCC 12228).";

Mol. Microbiol. 49:1577-1593(2003).

-!- FUNCTION: Transforms pimelate into pimeloyl-CoA (By similarity).

-!- CATALYTIC ACTIVITY: ATP + 6-carboxyhexanoate + CoA = AMP +

diphosphate + 6-carboxyhexanoyl-CoA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                            STRAIN=CV. Columbia,
STRAIN=CV. Columbia,
MEDLINE=2003487; PubMed=10617197;
MEDLINE=2003487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lini X., Kaul S., Rounsley S.D., Shea T.P., Benito M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pari G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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50.0%; Pred. No. 2.5e+02;
Pred. No. 2.5e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:-FINCTION: 3'-to-5' exoribonuclease specific for small oligoribonucleotides (By similarity).
-:- SIMILARITY: Belongs to the oligoribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Hydrolase; Exonuclease; Nuclease. ACT_SITE 148 148 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7126263D1E53D80E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B84667; B84667.
InterPro; IPR006055; Exonuclease.
Pfam; PF00929; Exonuclease; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AC005623; AAC77855.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 AA; 25737 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.vv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 LÉFISSDI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 XEFIXXDX 8
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STRAIN=ATCC 12228;
PubMed=12950922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1282;
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Venter J.C.;
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ID BIOW_STAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thaliana.";
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us-09-660-302e-1.rsp

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Query Match
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O9WZLZ:
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TIGR;
                                                                                                                                                                       THEMA
                                                                                                                                                RESULT 35
UBIE_THEMA
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Matches
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Welss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-ribose 5-phosphate = D-ribulose 5-phosphate.
-!- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.
-!- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 1; Length 228; 50.0%; Pred. No. 2.58+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              ; Score 25; DB 1; Length 229;
Pred. No. 2.5e+02;
4; Mismatches 0; Indels
  PATHWAY: Bioconversion of pimelate into dethiobiotin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
229 AA; 25194 MW; E6DDE60481159023 CRC64;
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                         SUBUNIT: Homodimer (By similarity).
SIMILARITY: Belongs to the biow family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Gr or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  EMBL; AE016744; AA003779.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF_00170; -; 1.
InterPro; IPR001034; HTH_DeoR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE010232; AAL81382.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF00455; deoR; 1.
ProDom, PD005813; RpiA, 1.
TIGRFAMS; TIGR00021; rpiA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004788; RpiA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :[|[::]:
LEFIKNDI 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus furiosus,
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPIA PYRFU
QBUIFO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAINHASBB / DSM 3109 / ATCC 43589;

MEDLINE=99287316; PubMed=10360571;

Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                           Menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 1; Length 22
50.0%; Pred. No. 2.5e+02;
ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 AA; 26494 MW; DCF6227D22A46DD5 CRC64;
                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                        229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the ubiE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_01813; -; 1.
InterPro; IPR001601; Methyltranef.
InterPro; IPR001601; SAM bind.
InterPro; IPR004033; UbiE/COG5_Metrf.
Pfam; PF01209; Ubie methyltran; 1.
PROSITE; PS01183; UBIE_1; FALSE_NEG.
PROSITE; PS01184; UBIE_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                      10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE001745; AAD35835.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Menaquinone biosynthesis;
                                                                                                                                                                                     STANDARD;
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                              :|||::|:
15 LEFIEDDM 22
                                                                                                                                                                                                                                                                                                                                                                        Thermotoga maritima.
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94 GEFIVGDA 101
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1 XEFIXXDX
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SEQUENCE 229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxiD=2336;
                                                                                                                                                                                                                                                                                                                                            JBIE OR TM0753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TM0753;
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YP07_MYCTU
ID YF07_MYCTU
AC P71786;
                                                                                                                                                                                  THEMA
                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
              NCBI TaxID=83557;
                                                                                                                                                                                     chlamydiaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHEL WCMVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potexvirus
                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                    MEDLINE=9895987; PubMed=9634230; Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Enonilingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                     PETRAIN=CDC 1551 / Oshkosh;
MEDLINE=2220644; PubMed=1218036;
Fleischmann R.D., Alland D., Bissen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Bissen J.A., Faft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 1; Length 231; 50.0%; Pred. No. 2.5e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculist, Rv1507c; -. Hypothetical proteome. SEQUENCE 231 AA; 27090 MW; BD18A247DB1B0BF8 CRC64;
       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Hypochetical protein Rv1507c/MT1555.
RV1507C OR MT1555 OR MTCY2777.29C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AE007023, AAK45820.1; -.
PIR, F70713, F70713.
TIGR, MT1555; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z79701; CAB02021.1; -.
                                                                                                                                                                                                                                                                                                                     complete genome sequence.";
Nature 393:537-544(1998).
                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PRI).
RPIA OR CCA00632.
Chlamydophila caviae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 DEFITYDD 32
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                        NCBI_TaxID=1773;
                                                                                                                                                                 STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPIA CHLCV
Q822P7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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0
                                                                                                                                                                                                                                                                                                                                                                                                      -:- CATALYTIC ACTIVITY: D-ribose 5-phosphate = D-ribulose 5-phosphate.
-:- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.
-:- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 16:291-303(1988).
--- FUNCTION: THIS PROTEIN MAY BE AN ATP-DEPENDENT HELICASE AND IS
REQUIRED FOR REPLICATION OF VIRAL DNA.
--- SIMILARITY: TO ORF2 FROM OTHER POTEXVIRUSES AND TO 25 kDa PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
STRAIN=GPIC;
MEDINE=2299155; PubMed=12682364;
MEDINE=2299155; PubMed=12682364;
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
Fraser C.M.;
                                                                                                                                                                                                                                                          GPIC):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88124202; PubMed=3340527;
Forster R.L.S., Bevan M.W., Harbison S.-A., Gardner R.C.;
"The complete nucleotide sequence of the potexvirus white clover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
                                                                                                                                                                                                                                                                                          examining the role of niche-specific genes in the evolution of
                                                                                                                                                                                                                                                          "Genome sequence of Chlamydophila caviae (Chlamydia psittaci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 1; Length 233; 50.0%; Pred. No. 2.5e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C0EDB3474B20A0C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR.1989 (Rel. 10, Created)
01-MAR.1989 (Rel. 10, Last sequence update)
01-0CT-1993 (Rel. 27, Last annotation update)
01-0CT-1993 (Rel. 27, Last annotation update)
White clover mosaic virus (strain M) (WCWV).
                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 31:2134-2147(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_00170; -; 1.
InterPro; IPR004788; RpiA.
ProDom; PD005813; RpiA; 1.
Isomerase; Complete proteome.
SEQUENCE 233 AA; 25544 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE016996; AAP05374.1; -.
TIGR; CCA00632; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM CARLAVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 EEFINTDL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 XEFIXXDX 8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=12189;
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                                                                                                                                                                                                                                                                                                         STRAINEATCS 35092 / DSM 1617 / P2;
STRAINEATCS 35092 / DSM 1617 / P2;
STRAINEATCS 35092 / DSM 1617 / P2;
She Qi, Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7846(2001).
                                                                                                                                                                                            Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mallet L., Bussereau F., Jacquet M.;
"A 43.5 kb segment of yeast chromosome XIV, which contains MFA2,
mP22, CAP/SRV2, NAM9, FKB1/FPR1/FBP1, MOM22 and CPT1, predicts an
adenosine deaminase gene and 14 new open reading frames.";
Yeast 11:1195-1209(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
4/pothetical 27.7 Kba protein in CPTI-SPC98 intergenic region.
VNL129W OR N1219 OR N1870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 1; Length 23 50.0%; Pred. No. 2.6e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01939; DUF91; 1.
ProDom; PD013521; DUF91; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 236 AA; 27264 MW; 6930125F102BBAC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the UPF0286 family.
         15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
1-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical UPF0286 protein SS02208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE006826; AAK42378.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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HAMAP, NF_00722; -; 1.
InterPro; IPR002793; DUF91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                               Sulfolobus solfataricus.
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224 LEFIRYDI 231
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                                                                                                                                                                                                                                                         NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=4932;
                                                                                                                                                                                                                               Sulfolobus.
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         DDT READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY READ DRY
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   (See http://www.isb-sib.ch/announce/
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SIMILARITY: TO ORF2 FROM OTHER POTEXVIRUSES AND TO 25 KDa PROTEIN
FROM CARLAVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Infectious transcripts and nucleotide sequence of cloned cDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         potexvirus white clover mosaic virus.";
Virology 177:152-158(1990).
-!- FUNCTION: THIS PROTEIN MAY BE AN ATP-DEPENDENT HELICASE AND IS
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MEDINE=90281578; PubMed=2353451;
Beck D.L., Forster R.L.S., Bevan M.W., Boxen K.A., Lowe S.C.,
Gardner R.C.;
                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 1; Length 236; 50.0%; Pred. No. 2.6e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 1; Length 236; 50.0%; Pred. No. 2.6e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                            49991932D8B6D4BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26451 MW; D470D75B46E9D418 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 14, Last sequence update) (Rel. 27, Last annotation update)
                                                                                                                                                                                                                                               (POTENTIAL)
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Pfam, PF01443; Viral helicasel.

DNA replication, ATP-binding; Helicase.

NP_BIND 28 35
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Probable helicase (ORF 2).
White clover mosaic virus (strain O) (WCMV).
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                                                                                                               PIR; S01086; S01086.
InterPro; IPR000606; Viral helicasel.
Pfam; PF01443; Viral helicasel; 1.
DNA replication; ATP-binding; Helicase.
NP_BIND 28 35 ATP (POTEN
                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                      236 AA; 26356 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
                                                                                      EMBL; X06728; CAA29905.1; -.
                                                                                                                                                                                                                                                                                                                                                                   50.08;
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entities requires a license
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Best Local Similarity 50.0%
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95 FEFIFTDP 102
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FEFIFTDP 102
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YMO8 SULSO
ID YMO8 SULSO
AC Q97WK8;
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VHEL WCMVO
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Gaps

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Length 236;

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Matches
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"Molecular characterization of the mitochondrial DNA of a new stopper mutant ER-3 of Neurospora crassa.";
Genetics 120:935-945(1988)
-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
chain that catalyzes the reduction of oxygen to water. Subunits 1-
3 form the functional core of the enzyme complex. Subunit 2
transfers the electrons from cytochrome c via its binuclear copper
A center to the binetallic center of the catalytic subunit 1.
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=83054012; PubMed=6291999; van den Boogaart P., van Dijk S., Agsteribbe E.; "The mitochondrially made subunit 2 of Neurospora crassa cytochrome aa3 is synthesized as a precursor protein."; FEBS Lett. 147:97-100(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c + 2 H(2)0.
COFACTOR: Copper A.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                            Length 240;
                                                                                                                                                                                                                                                             100.0%; Score 25; DB 1; Length 24:
50.0%; Pred. No. 2.6e+02;
w:=matches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cytochrome oxidase subunit 2 gene in Neurospora crassa
                                                                                                                                                                                                                                                SEQUENCE 240 AA; 27689 MW; F04E99885774CF53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytochrome c oxidase polypeptide II (EC 1.9.3.1) COX2 OR OXII.
                                                                                                                                                      PLIK; SSLACT, CREENCHING: 143135; -. SGD, SO005073; YNL129W.
InterPro; IRR000764; Uridine kin. PRINTS; PRO0988; URIDINKINASE.
PYPOthetical 12 20 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                       250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 258:13230-13235(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=84032555; PubMed=6313689;
Macino G., Morelli G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 01, Created)
(Rel. 01, Last sequ
(Rel. 41, Last anno
                                                                                                                  EMBL; Z46843; CAA86896.1; -. EMBL; Z71405; CAA96011.1; -.
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                                                                                                                                                                                                                                                                                                         4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                213 KEFINDDD 220
                                                                                                                                                 PIR; S55154; S55154.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion.
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                                                                                                                                                                     Electron transport; Respiratory chain.

DOMAIN 1 39 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97313264; PubMed=9169868; Dietrich F.S., Willigan J.T., Hennessy K.M., Yelton M.A., Allen E., Araujo R., Avil Mulligan D.T., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96086928; PubMed=7500933;
Hirayama T., Maeda T., Saito H., Shinozaki K.;
Cloning and characterization of seven cDNAs for hyperosmolarity-
responsive (HOR) genes of Saccharomyces cerevisiae.";
Mol. Gen. Genet. 249:127-138(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRIAL MATRIX (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 1; Length 250;
Pred. No. 2.7e+02;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COPPER A (PROBABLE).
COPPER A (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
GPP2 OR HOR2 OR YER062C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 AA
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28724 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             59
76
97
250
185
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STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|||::|:
137 DEFIEFDS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 AA;
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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GPP2_YEAST
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Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H. Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh. C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Weitstein D., Davis R.W., "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
                                                                                                                                                PARTIAL SEQUENCE, FUNCTION, AND CHARACTERIZATION.
MEDLINE=96278827; PubMed=8662716;
Norbeck J., Pachlman A.-K., Akhtar N., Blomberg A., Adler L.;
Norbeck J., Pachlman A.-K., Akhtar N., Blomberg A., Adler L.;
Norbeck J., Pachlman A.-K., Akhtar N., Blomberg A., Adler L.;
Norbeck J., Pachlman A.-K., Akhtar N., Blomberg A., Adler L.;
Dl.glycarol-3-phospharase from Saccharomyces cerevisiae.
Identification of the corresponding GPP1 and GPP2 genes and evidence for osmotic regulation of Gpp2p expression by the osmosensing mitogen-activated protein kinase signal transduction pathway.";
J. Biol. Chem. 271:13875-13881(1996).
                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Cytoplasmic.
INDUCTION: By osmotic stress.
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS DOGI, DOG2, GPP1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:000121; F:glycerol-1-phosphatase activity; IDA. GO; GO:0005975; P:carbohydrate metabolism; IDA. GO; GO:0005114; P:glycerol biosynthesis; IMP. GO; GO:0005970; P:response to osmotic stress; IDA. InterPro; IPR006402; HAD-SF-IA-v3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27814 MW; D69F343B10417313 CRC64;
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TIGRFAMS, TIGR01509, HAD-SF-IA-v3; 1.
Hydrolase, Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D50469; BAA09058.1; -.
EMBL; U18813; AAB64598.1; -.
                                                                                                            Nature 387:78-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S50565; S50565.
GermOnline; 139142; -.
SGD; S0000864; HOR2.
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                                                                                                                                                                                                                                                                                                                                                                           phosphate.
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TIGRFAMS;
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RESULT 45
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0
                                Gaps
                                ·;
; Score 25; DB 1; Length 250; Pred. No. 2.7e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                            250 AA
                                                                                                                                                          PRT;
                                                                                                                                                                                    (Rel. 41, Created)
(Rel. 41, Last seq
100.0%;
             50.0%;
                                                                                                                                                                                                                                                          Alder yellows phytoplasma.
                                                                                                                                                                                                                             30S ribosomal protein S3. RPSC OR RPS3.
                             4; Conservative
                                                                                                                                                         STANDARD;
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233 VEFIFDDY 240
                                                                                                                                                                                                                28-FEB-2003 (Rel. 41,
                                                        1 XEFIXXDX 8
           Best Local Similarity
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28-FEB-2003
                                                                                                                                                         RS3 ALDYE
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Matches

à qq Bacteria; Firmicutes; Mollicutes; Acholeplasmatales; Acholeplasmataceae; Phytoplasma. NCBI\_TaxID=72989;

RESULT 44
ID 3 ALDYE
ID 28-FE
DT 28-FE
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CS Alder
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[1] SEQUENCE FROM N.A. MEDLINE=22140588; PubMed=12144771;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
Martini M., Botti S., Marcone C., Marzachi C., Casati P., blanco F.A., Benedetti R., Bertaccini A.;
Benedetti R., martaccini A.;
"Genetic variability among flavescence doree phytoplasmas from different origins in Italy and France.";
Mol. Cell. Probes 16:197-208(2002)
-!-FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA in the 70S ribosome, positioning it for translation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=E.w.phytoplasma, and E.y.phytoplasma; STRAIN=ULW, and EY1; MEDLINE=22140589; PubMed=12144771; Marzachi C., Casati P., Bianco P.A., Benedetti M., Bortiscini A., Marcone C., Marzachi C., Casati P., Bianco P.A., "Genetic variability among flavescence doree phytoplasmas from different origins in Italy and France."; "Mol. Cell. Probes 16:197-208 (2002).

-: FUNCTION: Binds the lower part of the 30S subunit head, Binds mRNA in the 70S ribosome, positioning it for translation (By
                                                                                                                                                                                                                                                                  subunit. Forms a tight complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                        -1- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight cowith proteins 510 and 514 (By similarity).
-1- SIMILARITY: Belongs to the 53P family of ribosomal proteins.
-1- SIMILARITY: Contains 1 KH type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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Elm yellows phytoplasma.
Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ptam; Frust, KH; 1.
SMART; SM00322; KH; 1.
TIGREMS: TIGRO109; rpsC bact; 1.
PROSITE; PS50823; KH TYPE 2; 1.
PROSITE; PS00548; RIBOSOMĀL S3; 1.
Ribosomal protein; RNA-binding; rRNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEE-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (St or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF396936; AAL57324.1; -. HAMAP; MF 01309; -; 1. InterPro; IPR004087; KH dom. InterPro; IPR0040919; KH prok. InterPro; IPR001351; Ribosomal S3 C. InterPro; IPR001351; Ribosomal S3 C. InterPro; IPR005704; S3 bact. Pfam; PF00189; Ribosomal S3 C. Pfam; PF00189; Ribosomal S3 C. Pfam; PF00418; Ribosomal S3 C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acholeplasmataceae; Phytoplasma.
NCBI_TaxID=182216, 35774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 AA; 28367 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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65 DEFIEIDL 72
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es 4; Conserv
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                                                                                                                                                                                                                                similarity).
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Q8VLE1;
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similarity).
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                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAID=AL202, AT4, FD70, FD88, PC2, FN6, PV259, TV46, TV51, and VR2; STRAINE=Z2140588; DubMed=12144771; MEDLINE=Z2140588; DubMed=12144771; Marzini M., Botti S., Marcone C., Marzachi C., Casati P., Bianco P.A., Benedetti M., Bertaccini A.; "Genetic variability among flavescence doree phytoplasmas from different origins in Italy and France."; Mol. Cell. Brobes 16:197-208(2002).
-! FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA in the 70S ribosome, positioning it for translation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex with proteins 310 and 314 (By similarity).

with Approximation of the S3P family of ribosomal proteins.

-!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.

-!- SIMILARITY: Contains 1 KH type-2 domain.
              -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex with proteins S10 and S14 (By similarity).
-!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
-!- SIMILARITY: Contains 1 KH type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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InterPro; IPR008704; 83 bact.

R pfam; PF00189; Ribosomal_S3_C; 1.

R Pam; PF00189; Ribosomal_S3_N; 1.

R RMART; SM00322; KH; 1.

R TIGRPAMS; TIGR01009; rpsC bact; 1.

R PROSITE; PS00543; KH TYPE_2; 1.

DR PROSITE; PS00548; RIBOSOMAL_S3; 1.

Ribosomal protein; RNA-binding; rRNA-binding.

AMATN

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AMATS MW; 73E56A7E7819EAIA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 250;
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50.0%; Pred. No. 2.7e+02;
.ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
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STANDO STANDARU,
OBVIA2; OBVIA2; QBVIA3; OBVS62;
28-FEB-2003 (Rel. 41, Created Paguence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                  InterPro; IPR009019; KH_Drok.
InterPro; IPR004044; KH_TYPE_2.
InterPro; IPR001351; Kibosomal_S3 C.
InterPro; IPR008282; Kibosomal_S3_N.
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NCBI_TaxID=131152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flavescence doree phytoplasma.
                                                                                                                                                                                            EMBL; AF396949; AAL57337.1; -. EMBL; AF396938; AAL57326.1; -.
                                                                                                                                                                                                                                   InterPro; IPR004087; KH_dom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                         HAMAP; MF 01309; -; 1
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65 DEFIEIDL 72
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ID RS3_F
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Martini M., Botti S., Marcone C., Marzachi C., Casati P., Bianco P.A.,
Martini M., Botti S., Marcone C., Marzachi C., Casati P., Bianco P.A.,
Benedeti R., Bettaccini A.;
"Genetic variability among flavescence doree phytoplasmas from
different origins in Italy and France.";
Mol. Cell. Probes 16.197-208 (2002).
--- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA
--- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA
--- functions and propositioning it for translation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEMIN, FEVOTAL, ALLOSOMEAL_SS_A'; 1.

SMART; SM00322; KH; TPE_Z, 1.

PROSITE; PS50823; KH TYPE_Z; 1.

PROSITE; PS50823; KH TYPE_Z; 1.

PROSITE; PS00548; RIBOSOMĀL_S3; 1.

PROSITE; PS00548; RIBOSOMĀL_S3; 1.

PROSITE; PS00548; RIBOSOMĀL_S3; 1.

VARIANT 46 46 H -> Y (IN STRAINS AL202, AT4 AND PV259).

VARIANT 103 103 V -> I (IN STRAINS AL202, AT4, FD70 AND PV259).

VARIANT 118 118 V -> I (IN STRAINS TV46 AND TV51).

SEQÜENCE 250 AA; 28408 MW; E5441C224F164FF5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 25; DB 1; Length 25
Pred. No. 2.7e+02;
4; Mismatches 0; Indels
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Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
Acholeplasmataceae; Phytoplasma.
NCBI_TaxID=72996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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InterPro; IPR008282; Ribosomal S3_N.
InterPro; IPR008704; S3_bact.
Pfan; PF00189; Ribosomal S3_C; I.
Pfan; PF00187; Ribosomal S3_C; I.
                                                                                                                                                                                                                                             EMBL, AF396937, AAL57325.1; --
EMBL, AF396940, AAL57327.1; --
EMBL, AF396942, AAL57328.1; --
EMBL, AF396942, AAL57330.1; --
EMBL, AF396943, AAL57331.1; --
EMBL, AF396944, AAL57333.1;
EMBL, AF396947, AAL57335.1; --
EMBL, AF396950, AAL57335.1; --
EMBL, AF396950, AAL57335.1; --
EMBL, AF396950, AAL57338.1; --
EMBL, AF396951, AAL57338.1; --
EMBL, AF396951, AAL57338.1; --
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InterPro; IPR009019; KH prok.
InterPro; IPR004044; KH TYPE 2.
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65 DEFIEIDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAMAP; MF_01309; -; 1
InterPro; IPR004087;
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us-09-660-302e-1.rsp

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Benedetti R., Bertaccini A.,
"Genetic variability among flavescence doree phytoplasmas from
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--- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA
in the 70S ribosome, positioning it for translation (By
SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex
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                                         with proteins S10 and S14 (By similarity).
SIMILARITY: Belongs to the S3P family of ribosomal proteins.
SIMILARITY: Contains 1 KH type-2 domain.
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Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
Acholeplasmataccae; Phytoplasma.
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Pred. No. 2.7e+02;
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30S ribosomal protein S3.
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SEQUENCE FROM N.A.
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Mol. Biol. 208:587-599(1989).

-!-FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. Subunit 2 transfers the electrons from cytochrome c via its binuclear copper A center to the bimetallic center of the catalytic subunit 1.

-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome
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MEDLINE=90040693; PubMed=2530353;
Dyson N.J., Brown T.A., Ray J.A., Waring R.B., Scazzocchio C.,
Davies R.W.;
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Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 250;
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| InterPro; IPRO01351; Ribosomal S3_C. |
| InterPro; IPRO01351; Ribosomal S3_C. |
| InterPro; IPRO01892; Ribosomal S3_N. |
| InterPro; IPRO0189; Ribosomal S3_N. |
| InterPro; IPRO0189; Ribosomal S3_C. |
| Rem; PF00117; Ribosomal S3_C, 1. |
| SMART; SM00322; KH; 1. |
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| R PROSITE; PS50823; KH TYPE_2; 1. |
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28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome c oxidase polypeptide II (EC 1.9.3.1)
COX2 OR OXIB
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non-profit institutions as long
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50.0%; F
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Gene 98:107-112(1991).
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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Enviser L., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Brian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Briaseppi G., Buy B.J., Haga K., Halech J., Garlaci B.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Garadi G.,

RA Ghimseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Noris M., Levine A., Liu H., Masuda S., Kumano M.,

RA Norde D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Pottetelle D., Porwollik S., Perscott A.M.,

RA Sato T., Scanlan E., Schleich S., Schroete R., Scoffone F.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Takeuchi M., Tamakoshi A., Takagi T., Takabashi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Takagi T., Takabashi H., Vansiar Y.,

RA Takeuchi M., Tamakoshi A., Takagi T., Takagi T., Takagi T., Vansarotti A.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

RA Tosato V., Waller E., Wedler E., Wedler F., Vassarotti A.,

RA Viazi A., Wandutt R., Wedler E., Wedler H., Weitzenegger T.,
                                                                                                                                                                                                                                                                               MITOCHONDRIAL MATRIX (POTENTIAL).
POTENTIAL.
MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
COPPER A (PROBABLE).
                InterPro; IPR001505; Copper CuA.
InterPro; IPR008972; Cupredoxin.
InterPro; IPR008972; Cupredoxin.
InterPro; IPR008972; Cyf.c.ox_2.
Pfam; PF00116; COX2; 1.
Pfam; PF00116; COX2 TM; 1.
PRINTS; PR01166; CYCOXIDASEII.
PROSITE; PS000131; Copper CuA; 1.
PROSITE; PS00079; COX2; 1.
Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                 MÍTOCHONDRIAL INTERMEMBRANE (POTENTIAL) POTENTIAL.
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Pred. No. 2.8e+02;
4; Mismatches 0; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-WAY-2000 (Rel. 39, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Hypothetical protein yoxB (ORFI19+).
                                                                                                                                                                                                                        Respiratory chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
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(Rel. 39, Last seqn
(Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                              28930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
  EMBL; X15441; CAA33481.1; -.
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105
252
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137 NEFIEFDS 144
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60
106
1106
219
223
223
223 AA;
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Best Local Similarity
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01-DEC-1992 (Rel
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STRAIN—SATCC 35092 / DSM 1617 / P2;
STRAIN—SATCC 35092 / DSM 1617 / P2;
She Q., Singh R.K., Confaionieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
The complete genome of the cremarchaeon Sulfolobus solfataricus P2.",
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.; "Sequence analysis of the Bacillus subtilis chromosome region between the terC and odhAB loci cloned in a yeast artificial chromosome."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                       Ann K.S. Wake R.G. Ann K.S. Wake R.G. Ann K.S. Wather social features of the sequence spanning the replication terminus of Bacillus subtilis 168 and W23 chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable diphthine synthase (EC 2.1.1.98) (Diphthamide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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50.0%; Pred. No. 2.8e+02;
.ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M24523; -; NOT ANNOTATED_CDS.
EMBL; M24523; -; NOT ANNOTATED_CDS.
EMBL; AF027868; AAB84418.1; -.
PIR; B69930; B69930.
Subtlist; BG11046; yoxB.
Hypothetical protein; Complete proteome.
SEQUENCE 256 AA; 28452 MW; B9B64B0BECEOAB3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 AA
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91192601; PubMed=1849493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 72-256 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z99114; CAB13745.1; -.
                                                                                                                                                                                                                                                                      SEQUENCE OF 1-119 FROM N.A.
                                                                                                                                                                               Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 50.0
Matches 4; Conservative
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STRAND
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SEQUENCE FROM N.A.
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STAIN-LIZE / SGSG1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., RA Waterston R., Wilson R.K.;
RA Materston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                  Gaps
biosynthesis (By similarity).
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 2-(3-carboxy-3-aminopropyl)-L-histidine = S-adenosyl-L-homocysteine + 2-[3-carboxy-3-(methylameonio)propyl]-L-histidine + 2-[3-Carboxy-3-(methylameonio)propyl]-L-histidine.
PATHWAY: Diphthamide biosynthesis; second step.
SIMILARITY: Belongs to the diphthine synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TWO Periprasmic transport proteins which interact with a common membrane receptor show extensive homology: complete nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                    LO-CEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last amnotation update)
Lysine-arginine-ornithine-binding periplasmic protein precursor
ARGT OR SIM2355.
                                                                                                                                                                                                                                                                                                                   ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92084686; PubMed=1748660;
Kang C.-H., Shin W.-C., Yamagata Y., Gokcen S., Ames G.F.-L.,
Kim S.-H.;
                                                                                                                                                                                                                                                                                        ; Score 25; DB 1; Length 257; Pred. No. 2.8e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=82082392; PubMed=6273842;
Higgins C.F., Ames G.F.-L.;
"Two periplasmic transport proteins which interact with
                                                                                                                                                                                                                                                        ; Complete proteome.
218BE19B593BF01B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 78:6038-6042(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                    260 AA.
                                                                                                                                                                                PIR; D90246; D90246.
HAMAP; MF 01084; -; 1.
InterPro; IPR000878; Cor/por_Metransf.
InterPro; IPR004551; Dphthn_synthase.
Ffam; PF00590; TP methylase; 1.
Transferaes, Methyltransferaes; Complete SEQUENCE 257 AA; 28834 MW; 218BB19B5s
                                                                                                                                                                        EMBL; AE006715; AAK41227.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                          100.08;
                                                                                                                                                                                                                                                                                                    50.08;
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.00,
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                 Kim S.-H.;
J. Belongs to the bacterial extracellular solute-binding
                                                                                         MEDLINE=93266593; PubMed=8496186;
Oh B.-H., Pandit J., Kang C.-H., Nikaido K., Gokcen S., Ames G.F.-L.,
                                                                                                                                                                                                                                                                 B.-H., Pandit J., Kang C.-H., Nikaido K., Gokcen S., Ames G.F.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIGRFAMS, TIGR01096, 3A0103803R, 1.
PROSITE; PS01039; SBP_BACTERIAL_3; 1.
Transport; Amino-acid transport; Periplasmic; Signal; 3D-structure;
"Crystal structure of the lysine-, arginine-, ornithine-binding protein (LAO) from Salmonella typhimurium at 2.7-A resolution."; J. Biol. Chem. 266:23893-23899(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYSINE-ARGININE-ORNITHINE-BINDING
                                                                                                                                                   "Three-dimensional structures of the periplasmic
lysine/arginine/ornithine-binding protein with and without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERIPLASMIC PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stydene; Sclool8; argr.
InterPro; IPRO05768; Lys Arg Orn bind.
InterPro; IPRO01311; SBP/glurreceptor.
InterPro; IPRO01638; SBP bac 3.
Pfam; PF00497; SBP bac 3; 1.
                                                                         K-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                           Biol. Chem. 268:11348-11355(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; V01368; CAA24651.1; -.
EMBL; J01805; AAA75577.1; -.
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PDB; 2LAO; 22-JUN-94.
PDB; 1LAF; 10-JUL-95.
PDB; 1LAG; 10-JUL-95.
PDB; 1LAG; 10-JUL-95.
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SOLUTION SELLA SEL

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Escherichia coli.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blattner F.R.;
"Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGGSSAAGT -> TGASGGSSA (IN REF. 3).
MISSING (IN REF. 3).
N -> D (IN REF. 3).
MISSING (IN REF. 3).
D73852833694C6E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 260;
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Pred. No. 2.9e+02;
4; Mismatches 0; Indels
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STRAIN=K12 / MG4655,
MEDLINE=95334362; Plunkett G. III, Sofia H.J., Daniels D.L.,
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                            -!- SIMILARITY: Belongs to peptidase family A4
                                                                                                                                                                                                                                                                                                                                        Hydrolase, Aspartyl protease, Zymogen, Signal.
SIGNAL 1 20 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
FHUF OR B4367.
                                                                                                                                                                                                                                                                                                                                                                               SCYTALIDOPEPSIN
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                                                                                                                                                                                                                                                                                       InterPro, IPR000250; Peptidase_A4.
Pfam; PF01283; Peptidase_A4; 1.
PRINTS; PR0097; SCYILDPTASE.
ProDom; PD018627; AspproteaseA4; 1.
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Maita T., Nagata S., Matsuda G., Maruta S., Oda K., Murao S.,
Tsuru D.; "Complete amino acid sequence of Scytalidium lignicolum acid protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid
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MEDLINE=98430139; PubMed=9757573;

Moda N., Gorch Y., Oyama H., Murao S., Oda K., Tsuru D.,

"Nucleotide sequence of the gene encoding the precursor protein of peptratin insensitive acid protease B, scytalidopepsin B, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P15369; Q92333; Q9P962;
01-APR-1990 (Rel. 14, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Scytalidopepsin B precursor (EC 3.4.23.32) (Acid protease B) (SLB)
Scytalidium lignicolum.
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SEQUENCE OF 50-260 FROM N.A.
MEDLINE=96376187; PubMed=8782420;
Kakimori T., Yoshimoto T., Oyama H., Oda N., Gotoh Y., Oda K.,
                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 1; Length 260;
Pred. No. 2.9e+02;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scytalidium lignicolum.";
Biosci. Biotechnol. Biochem. 62:1637-1639(1998)
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1; Mismatches
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50.08; File
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46 GEFIGFDI 53
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      PRTB SCYLI
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PRTB_SCYLI
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0
                                                                                                                           of 2Fé-2S center.";
Bur. J. Biochem. 258:1001-1008(1998).
-!- FUNCTION: Involved in the reduction of ferric iron in cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence features of the regions of 1,381,565 bp covered by twenty one physically assigned P1 and TAC clones."; DNA Res. 5:131-145(1998).
                                                                 Muller K., Matzanke B.F., Schunemann V., Trautwein A.X., Hantke K., "FnuF, an iron-regulated protein of Escherichia coli with a new type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                              COFACTOR: Binds 1 2Fe-2S cluster. SUBCELLULAR LOCATION: Cytoplasmic; sometime membrane-associated.
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STRAIN=cv. Columbia;
MEDLINE=98344145; PubMed=9679202;
Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=21016721; PubMed=11130714;
MEDLINE=21016721; PubMed=11130714;
Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu B.,
Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
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Pred. No. 2.9e+02;
4; Mismatches 0; Indels
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EMBL; AE00500; ...

RPI; S6594.

RECOGENE; EQ1259; fluf.

DR PRINTS; PR01714; 2FB2SRDCTASE;

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244 24 1RON-SULFUR (2FE-2S).

RINON-SULFUR (2FE-2S).

1RON-SULFUR (2FE-2S).
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CHARACTERIZATION.
MEDLINE=99144129; PubMed=9990318;
Muller K., Matzanke B.F., Schunem
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SEQUENCE FROM N.A.
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P4 20
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DT 15-MAI
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A Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
A Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
A Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
Stoneking T., Pepin K., Spieth J., Scakhon M., Armstrong J., Becker M.,
Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
A Belter E., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,
RA Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,
RA Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.A.,
RA Wolckaert G., Wambut R., Duesterhoeft A., Stiekema W., Pohl T.,
RA Wolckaert G., Wambut R., Duesterhoeft A., Stiekema W., Pohl T.,
RA Samsperger U., Wedler H., Balke K., Weler E., Johnson S.,
Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
RA Weitzenegger U., Wedler H., Balke K., Weler E., Jehnson S.,
Weitzenegger U., Wedler H., Balke K., Weler E., Jehnson S.,
RA Weitzenegger T., Bohthe G., Rose M., Hauf J., Berneiser S., Hempel S.,
Reldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
RA Schueller C., Zaccaria P., Mewes H. W., Bevan M., Fransz P.F.;
RA Schoef H.,
RR Schueller C., Zaccaria P., Mewes H. W., Bevan M., Fransz P.F.;
RT Lealiana ".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. Columbia,

MEDLINB=22954850; PubMed=14593172;

MEDLINB=22954850; PubMed=14593172;

Wamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

Warlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Ouach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

Miranda M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao O., Croy N., Bilu A., Goldsmith A.D., Gurial M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Saki M., Sakurai T.,

Satou M., Tamse R., Vaysberg M., Wallender E.K., Hong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delseny M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia;
Philipps G., Gigot C.;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Cv. Columbia;
Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., De
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Columbia;
Cooke R., Laudie M., Raynal M., Delseny M.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 408:823-826(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene model prediction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                  SPECIES=E.coli;
MEDLINE=89136010; PubMed=2645057;
de Boor P.A.J., Crossley R.E., Rothfield L.I.;
da Boor p.A.J., crossley R.E., Rothfield L.I.;
by the minicell locus determine proper placement of the division septum in B. coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-FBE-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Septum site-determining protein minD (Cell division inhibitor minD).
MIND OR B1175 OR C1622 OR Z1937 OR ECS1669 OR SF1162 OR S1248.
Bscherichia coli 06,
Escherichia coli 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=E.coli; STRAIN=K12 / MG1655; MEDLINE=97426617; PubMed=9278503; Blattner F. R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacieria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
                                                                                                                                                                                                                                                                                                                                                                         Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Ross
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                        ; Score 25; DB 1; Length 26
Pred. No. 2.9e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                              61B8E1C557CC5485 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 AA
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SPECIES-E.coli; STRAIN-K12;
MEDLINE-97061202; PubMed-8905232;
                                                                                                                                                                                                                                                                                                                                   DRBM
                                                                                                                                                                                                                                                                                                                                                 30224 MW;
                                                                                                                          EMBL; AP001515; BAB06208.1; -.
                                                                                                                                                                                                                                                                                                                                                                              100.08;
                                                                                                                                                                                                                                                                                                                                                                                             50.08;
                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 56:641-649(1989).
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196 QEFIQRDN 203
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 XEFIXXDX 8
                                                                                                                                                                                                                                                                                                                                                  263 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shigella flexneri.
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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MIND ECOLI
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             entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            halodurans and genomic sequence comparison with Bacillus subtilis.", Nucleic Acids Res. 28:4317-433 (2000).
-!- FUNCTION: Digests double-stranded RNA. Involved in the processing of ribosomal RNA precursors and of some mRNAS (By similarity).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphomonoester.
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
---- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
---- SIMILARITY: Contains 1 RNase III domain.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE 225 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
MEDLINE=20512582; PubMed=11058132;
MEDLINE=20512582; PubMed=11058132;
MEDLINE=20512582; Nakamura Y., Maeno G., Sasaki R., Masui N., Fuji P., Hirama C., Nakamura Y., Ggasawara N., Kuhara S., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
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Pred. No. 2.9e+02;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                A -> G (IN REF. 5).
P -> S (IN REF. 5).
R -> M (IN REF. 5).
A -> S (IN REF. 5).
I -> IV (IN REF. 6).
AS -> SA (IN REF. 6).
W, EF0847171FP9CA67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease III (RC 3.1.26.3) (RNase III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 2.9e+v
50.0%; Pred. No. 2.9e+v
... 4; Mismatches
                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00528; RIBOSOMAL_S4E; 1.
PROSITE; PS50889; 84; 1.
Ribosomal protein; RNA-binding.
DOMAIN 42 104 84 RNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 AA
                             or send an email to license@isb-sib.ch)
                                                       EMBL, AB010697; BAB11167.1; ALT_SEQ. EMBL; AY050933; AAK9350.1; -. EMBL; AY050933; AAK93510.1; -. EMBL; Z17994; CAA79086.1; ALT_INIT. EMBL; Z32619; CAA83563.1; -. EMBL; Z32619; CAA83562.1; -. EMBL; T28499; CAA79206.1; -. EMBL; T48480; T48480. InterPro; IPR005824; XOW.
                                                                                                                                                                                                                                                   Pfam; PF00467; KOW; 1.
Pfam; PF00900; Ribosomal_S4e; 1.
Pfam; PF01479; S4; 1.
Problom; PD002667; Ribosomal_S4E; 1.
SMART; SM00739; KOW; 1.
                                                                                                                                                                                                        InterPro; IPR00646; KOW sub.
InterPro; IPR000876; Ribosomal_S4E.
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                                                                                                                                                                                                                                        InterPro; IPR002942; S4.
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RNC OR RNCS OR BH2489.
Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | | :: |:
170 VEFIKFDV 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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31
53
53
92
92
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Q9KA05;
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Gaps

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us-09-660-302e-1.rsp

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Infect. Immun. 71:2775-2786(2003)
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                                           SO THE HING WE HERE HERE HERE HERE COULD COULD COURTER WELFT WE WERE THE WARRE TO SO THE SOURCE SOURCE THE SOURCE 
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Moromura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SPECIES-E.COl; STRAIN=06:H1 / CFT073 / ATCC 700928;

MEDLINE=2238824; PubMed=12471157;

Welch R.A., Burland V., PubMett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;

MEDLINE-21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Kulara S., Shiba T., Hantori M., Shinagawa C., Ogasawara N., Yasunaga T., Kulara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
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MEDLINE=2272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli "K-12.";
Electrophoresis 18:1259-1313 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES—B. coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=22074995; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Potcheck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
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                                                                                                                                                                                               Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
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MEDLINE=22590274; PubMed=12704152;
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MEDLINE=97443975; Pubmed=9298646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:529-533(2001).
                                                                                                                                                   Sampei G., Seki Y., Ta
Yano M., Horiuchi T.;
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                                                                                                                                                                                                                                                                                                 Raskin D.M., de Boer P.A.;

"Rapid pole-to-pole oscillation of a protein required for directing division to the middle of Escherichia col;";

Proc. Natl. Acad. Sci. U.S.A. 96:4971-4976 (1999)

-!- FUNCTION: APPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE DIVISION SITE. CELL DIVISION INHIBITORS MINC AND MIND ACT IN CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE FOLES OF THE CELL TO DESTABLILIZE FYZZ FILAMENTS THAT HAVE FORMED BEFORE THEY MATURE INTO POLAR Z RINGS.
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                                                                                 de Boer P.A.J., Crossley R.E., Hand A.R., Rothfield L.I.; "The MinD protein is a membrane ATPase required for the correct placement of the Escherichia coli division site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-SS: LESS EFFECTIVE THEN WILD-TYPE. K->Q: LOSS OF ACTIVITY. KT->QR: LOSS OF ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBDATT: Interacts with minC and ftsZ.
-!- SUBCELLULAR LOCATION: Inner membrane-associated.
-!- SIMILARITY: Belongs to the parA family. MinD subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell division; Septation; ATP-binding; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0DIB29A476A190B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3e+02;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL)
                                                                                                                                                                                                                                            SPECIES=E.coli;
MEDLINE=99238467; PubMed=10220403;
FUNCTION, AND MUTAGENESIS.
SPECIES=E.coli;
MEDLINE=92097557; PubMed=1836760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003348; Arsa ATPase.
InterPro; IPR000707; ATPase_ParA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE016759, AAN800871,
EMBL, AE003334, AAG56026.1;
EMBL, AP0022555, BAB35092.1;
EMBL, AE016142; AAN42779.1;
EMBL, AE016982; AAP16670.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 AT
14 G-
15 K-
16 KT
29483 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02374; ArsA_ATPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J03153; AAB59062.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000216; AAC74259'1; -
EMBL; D90751; BAA36009.1; -
EMBL; D90752; BAA36022.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; B31877; CCECID.
PIR; E90837; E90837.
PIR; P85695; P856937.
SWISS-2DPAGE; P18197; COLI.
ECOGene; EG10597; minD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%;
                                                                                                                                                                     EMBO J. 10:4371-4380(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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113 FEFIVCDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00991; ParA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                        CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGEN
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01-AUG-1990 01-AUG-1990

P16598

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MEDILINE=85240547; PubMed=2989698; March C.J., Mosley B., Larsen A., Cerretti D.P., Braedt G., Price V., March C.J., Mosley B., Larsen A., Cerretti D.P., Grabstein K., Conlon P.J., Gills S., Henney C.S., Kronheim S.R., Grabstein K., Cosman D.; Hopp T.P., Cosman D.; "Cloning, sequence and expression of two distinct human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND VARIANT SER-114.
MEDLINE=90249285; PubMed=2035664;
Kotenko S.V., Bulenkov M.T., Velko V.P., Epishin S.M., Lomakin I.B., Emel'Yanov A.V., Kozlov A.P., Konusova V.G., Kotov A.Y., Kallov A.P., Konusova V.G., Kotov A.Y., Ventatova T.V., Reshetnikov V.L., Simbirtsev A.S., Ketlinskii S.A., Vinetskii Y.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=8641855; PubMed=3485152;
MEDLINE=8641855; PubMed=3485152;
Gubler U., Chua A.O., Stern A.S., Hellmann C.P., Vitek M.P.,
Dechiara T.M., Benjamin W.R., Collier K.J., Dukovich M.,
Pamilletti P.C., Fiedler-Nagy C., Jenson J., Kaffek K., Kilian P.L.,
Stremlo D., Wittreich B.H., Woehle D., Mizel S.B., Lomedico P.T.,
"Recombinant human interleukin 1 alpha: purification and biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.L., Feingold E.A., Grouse D.H., Derge J.G., Strausberg R.L., Feingold E.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANTS GLN-85; SER-114 AND ASN-138. Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A., Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=81156769; PubMed=3493774;
Nishida T., Nishino N., Takano M., Kawai K., Bando K., Masui Y.,
Nakai S., Hirai Y.,
                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning of the cDNA coding for human prointerleukin-1 alpha and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakai S., Hirai Y., "CDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                      Furutani Y., Notake M., Fukui T., Ohue M., Nomura H., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete nucleotide sequence of the gene for human interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANT SER-114.
MEDLINE-85297782; PubMed=2994016;
Furuteni Y., Nortake M., Yamayoshi M., Yamagishi J., Nomura H.,
Ohue M., Furuta R., Fukui T., Yamada M., Nakamura S.;
"Cloning and characterization of the cDNAs for human and rabbit
                Interleukin-1 alpha precursor (IL-1 alpha) (Hematopoietin-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 143:345-352(1987).
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prointerleukin-1 beta.";
Dokl. Akad. Nauk SSSR 309:1005-1008(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 14:3167-3179(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-1 precursor.";
Nucleic Acids Res. 13:5869-5882(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=86205226; PubMed=3486405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunol. 136:2492-2497(1986).
                                                                                                                                                                                                                                                                                                                                                   Nature 315:641-647(1985).
                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                complementary DNAs.
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakamura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                THYMOCYTE PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.

IL-1 PROTEINS ARE INVOLVED IN THE INPLAMMATORY RESPONSE, BEING IDENTIFIED AS ENDOGENOUS PROGENS, AND ARE REPORTED TO STIMULATE INDENTIFIED TO STIMULATE SUBUNIT: MONOMEY.

SUBUNIT: MONOMEY.

DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE MISSELLANDOUS SERVE SOME AS YET UNDEFINED FUNCTION. MISSELLANDOUS: THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION. MISSELLANDOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGNENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS.

OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                             Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                             MEDLINE=89278054; PubMed=2471704;
Nishida T., Nishino N., Takano M., Sekiguchi Y., Kawai K.,
Misuno K., Nakai S., Masui Y., Hirai Y.;
"Molecular cloning and expression of rat interleukin-1 alpha cDNA.";
J. Biochem. 105.351-357(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERLEUKIN-1 ALPHA.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
E3BE22F576F291DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P01583; 1ITA.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR008905; III_propep.
InterPro; IPR000975; Interleukin_1.
Pfam; PF00340; III; 1.
Pfam; PF00344; III. propep; 1.
SMART; SM00125; III. 1.
PROSITE; PS00253; INTERLEUKIN 1; 1.
Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 25; DB 1; Length 270;
Pred. No. 3e+02;
4; Mismatches 0; Indels
                                                                                                     Interleukin-1 alpha precursor (IL-1 alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01, Created)
01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECRETORY PROTEINS. SIMILARITY: Belongs to the IL-1 family.
                270 AA
                                                       (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 37, Last annotation update
                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30856 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D00403; BAA00306.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114
                                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEFIMNDS 141
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                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139
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21-JUL-1986 (
21-JUL-1986 (
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IL1A HUMAN ID TL1A HUMAN

RESULT 59

134

엄

CARBOHYD SEQUENCE CARBOHYD

PROPEP

Match

Query Best L

Matches

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Progression M. Morson R., Barnes A.A., Rubin G.M., Homg L.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Peters G.J., Abruson B. B.,
Rada S., Loquellano N.A., Soldano J. Schmitt J. Mygres R.M., Glubs B.,
Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Sanche A.,
Rodizage A.C., Grimwood J., Schmitt J. Wygres R.M.,
Rodizage A.C., Grimwood J., Schmitt J. Mygres R.M.,
Rodizage A.C., Grimwood J., Schmitt J. Mygres R.M.,
Rodizage A.C., Grimwood J., Schmitt J. Mygres R.M.,
Rodizage R.M., Mygran J. R., Schale S., Sanch S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S., Rada S.,
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Gaps
MIM; 147760; -.

GO; GO:0005515; C:extracellular space; TAS.
GO; GO:0005125; F:cytokine activity; TAS.
GO; GO:0004971; F:signal transducer activity; TAS.
GO; GO:0004971; F:signal transducer activity; TAS.
GO; GO:0006916; P:antl-apoptosis; TAS.
GO; GO:0008283; P:inflammatory response; TAS.
GO; GO:0008285; P:inflammatory response; TAS.
GO; GO:0008285; P:inflammatory response; TAS.
InterPro; IPR008996; Cytok_III_like.
InterPro; IPR008996; Cytok_III_like.
InterPro; IPR009975; Interleukin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                       Pfam; PF00340; ILI; 1.
Pfam; PF00294; ILI; propep; 1.
SMART; SM00125; ILI; 1.
PROSITE; PS00255; INTERLEUKIN 1; 1.
Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Interleukin-1 alpha precursor (IL-1 alpha) (Hematopoietin-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 1; Length 271;
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D -> H (in dbsNP:1801715).
/FTId=VAR_014601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R -> 0.
/FTId=VAR_014304.
A -> S (in_dbSNP:17561).
/FTId=VAR_014305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N -> D (in dbSNP:17562)
                                                                                                                                                                                                                                                                                                                                                                                             N(6)-myristoyl lysine.
N(6)-myristoyl lysine.
N-LINKED (GLCNAC. ..)
                                                                                                                                                                                                                                                                                                                                Polymorphism; 3D-structure; Myristate; Lipoprotein.
PROPEP
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Best Local Similarity 50.0
Matches 4; Conservative
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132 YEFILNDA 139
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AC P79340;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                          DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO ENDS OF THESE PROPEINS SERVE SOME AS YET UNDEFINED FUNCTION. MISCELLANGOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS PRECURSOR SEQUENCE AMERICANISM DIPPERING FROM THAT USED FOR OTHER
                                                                                J. IMMUNDOL. 155:3946-3954 (1995).

J. IMMUNDOL. 155:3946-3954 (1995).

J. IMMUNDOL. BRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
-!- FUNCTION: PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.

IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
                         "Comparative sequence analysis of cytokine genes from human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Inflammatory response; Pyrogen.
BY SIMILARITY.
Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 271;
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tyrosinase (EC 1.14.18.1) (Monophenol monooxygenase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERLEUKIN-1 ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; Db 1, No. 3e+02;
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the IL-1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR003502; IL1 propep.
InterPro; IPR000975; Interleukin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEam; PF00340; ILL; 1.
Pfam; PR00394; ILL] PrOPEP; 1.
SMART; SM00125; ILL; 1.
PROSITE; PS00253; INTERLEUKIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine; Macrophage; Mitogen;
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HSSP; P01583; 11TA.
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132 HEFILNDT 139
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                                                                         nonhuman primates.";
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MELC2 OR MEL.
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                                                                                                                Subjected (JAN-1997) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

-!- PUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE B-CELL

MATURATION & PROLIFERATION BY INDUCING IN THE INFLAMMATORY RESPONSE, BEING

IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING

IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING

IL-1 PROTEINS ARE DINOCHOUS PYROGENS, AND ARE REPORTED TO STIMULATE

-!- SUBUNIT: MONOMER.

-!- SUBUNIT: MONOMER.

-!- DOWAIN: THES SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE

ANINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDERFINED FUNCTION.

-!- MISCELLANBOUGS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE

PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS

OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL) (POTENTIAL) (POTENTIAL) .
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Pfam; PF00340; IL1; 1.
Pfam; PF00344; IL1 propep; 1.
SMART, SMO0125; IL1; 1.
PROSITE; PS00255; INTERLEUKIN 1; 1.
PROSITE; PS00255; MITOGEN; Inflammatory response; Pyrogen.
""Ackine; Macrophage; Mitogen; Inflammatory response; Pyrogen.""" (POTENTIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Interleukin-1 alpha precursor (IL-1 alpha) (Hematopoietin-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25; DB 1; Length 271; red. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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N-LINKED (GLCNAC. .) (POT
N-LINKED (GLCNAC. .) (POT
W; 0526A9A6404558F0 CRC64;
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i; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the IL-1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR008996; Cytok ILI like.
Interpro; IPR003502; ILI propep.
Interpro; IPR000975; Interleukin_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30685 MW;
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132 HEFILNDT 139
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                                                                                         SEQUENCE FROM N.A.
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                            NCBI_TaxID=9541;
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CARBOHYD CARBOHYD SEQUENCE Query Match

CARBOHYD

Matches

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P48089

RESULT 61 IL1A MACMU

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Gaps

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1 XEFIXXDX 8
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Best Local Similarity
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P55022;
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SEQUENCE
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                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                     THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yung Z.-H., Zhao G.-F., Qu D., Danchin A., Wen Y.-M.; Chen Z., "Genome-based analysis of virulence genes in a non-biofilm-forming Staphylococcus epidermids strain (ATCC 12228) ", "Mol. Microbiol 49:1577-1593(2003) ". CATALYTIC ACTIVITY: ATP + deamido-NAD(+) + NH(3) + H(2)O = AMP
  THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·
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                                                                        CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA + DOPAquinone + H(2)O. COFACTOR: Binds 2 copper ions per subunit (By similarity). SIMILARITY: Belongs to the tyrosinase family.
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Pred. No. 3e+02;
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COPPER A (BY SIMILARITY).
COPPER B (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBCNPI; 2/5 AA. 15-MAR-2004 (Rel. 43, Created) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) NH(3) -dependent NAD(+) synthetase (EC 6.3.5.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 3e+0
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR008922; Di-Copper centre.
InterPro; IPR002627; Tyrosinase.
PERM; PR00264; tyrosinase; 1.
PRINTS; PR00092; TYROSINASE; PROSITE; PS00497; TYROSINASE 1; 1.
PROSITE; PS00498; TYROSINASE 2; 1.
Melanin biosynthesis; Oxidoreductase; Moi INIT MET 0 0 BY SIMILARI'
METAL 36 36 COPPER A (BR
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-!- PATHWAY: NAD biosynthesis.
-!- SIMILAPTTV.
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52
61
188
192
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37 NEFIVADT 44
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STRAIN=ATCC 12228;
PubMed=12950922;
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NADE STREP
1D ANDE STREP
AC QBCNF1;
DT 15-MAR-2004
DT 15-MAR-2004
DT 15-MAR-2004
DT 15-MAR-2004
DT 15-MAR-2004
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DT 15-MAR-2004
DT 15-MAR-2004
RN NCBL TAXID=1;
RN SEQUENCE FROM RCB STRAIN=ATCC
RX PubMed=12950;
RX PubMed=12950;
RX AVAN Z.-Q.,
RA YUAN Z.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DSM 40480;
Whiteles U.F., Brass N., Roessler C., Piepersberg W.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
                                                                                                                                                                                                                                                                                                                          Gaps
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-!- COFACTOR: Binds 2 copper ions per subunit (By similarity).
-!- SIMILARITY: Belongs to the tyrosinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces,
                                                                                                                                                                                                                                                                                   Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monooxygenase; Copper.
                                                                                                                                                                                                                                                                                                                      0; Indels
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BY SIMILARITY.
; CF4B22401F9F77D9 CRC64;
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COPPER A (BY SIMILARITY).

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01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Tyrosinase (EC 1.14.18.1) (Monophenol monooxygenase).
                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; 50.0%; Pred. No. 3.1e+02; ative 4; Mismatches 0
                                                                          EMBL, AE016749; AAO05195.1; -.
HAMAPP, MF 00193; -; 1.
ILITETPO.; IPR003694; NAD synthase.
Pfam; PF02540; NAD synthase; 1.
TIGRPAMS; TIGR0552; nadE; 1.
LIGRSE, ATP-binding; Complete proteome.
NP_BIND 47 54 ATP (BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, X95705, CAA65005.1; -. InterPro; IPR00892; Di-copper centre. InterPro; IPR00822; Di-copper centre. Francis Proud. 1 Profusiase; IPR00264; Lyrosinase; IPR01818; PR0092; TYROSINASE. PROSITE; PROSITE; PS00497; TYROSINASE. PROSITE; PS00499; TYROSINASE. PALSE NEG. Melanin blosynthesis; Oxidoreductase; Monoox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                       275 AA; 30880 MW;
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                                                                                                                                                                                                                                                                                                                                                                              : | | | :: |:
97 LEFINPDT 104
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275 AA;
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STANDARD;
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Best Local Similarity
                                                       FROM N.A.
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-!- CATALYTIC ACTIVITY: ATP + deamido-NAD(+) + NH(3) + H(2)O = AMP +
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
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                              ; Score 25; DB 1; Length 275; Pred. No. 3.1e+02; 4; Mismatches 0; Indels
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-!- PATHWAY: NAD biosynthesis.
-!- SIMILARITY: Belongs to the NAD synthetase family.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1)
NADE OR CGL2534.
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                                                                                                                                                                                                                                                                                                                                                                     277 AA
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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38 NEFIMSDT 45
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Bidwai A.P., Reed J.C., Glover C.V.C.;

Biochem Kinse II of Saccharomyces cerevisiae contains two distinct regulatory submits, beta and beta.";

Arch. Biochem. Biophys. 309:348-355(1994).

-!- FINGTION: Plays a complex role in regulating the basal catalytic activity of the alpha submint (By similarity).

-!- SUBUNIT: Tetramer composed of an alpha chain, an alpha', one beta chain and one beta chain.

-!- FINK: Phosphorylated by alpha chain (By similarity).

-!- SIMILARITY: Belongs to the casein kinase 2 beta chain family.
                   Bidwai A.P., Reed J.C., Glover C.V.C.; 
"Cloning and disruption of CKB1, the gene encoding the 38-kDa beta 
"Cloning and disruption of CKB1, the gene encoding the 38-kDa beta 
subunit of Saccharomyces cerevisiae casein kinase II (CKII). Deletion 
of CKII regulatory subunits elicits a salt-sensitive phenotype."; 
J. Biol. Chem. 270:10395-10404 (1995).
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SEQUENCE 278 AA; 32265 MW; 9ACA8D285E6990AF CRC64;
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Pred. No. 3.1e+02;
4; Mismatches 0; Indels
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS01101; CK2_BETA; 1.
MEDLINE=95256195; PubMed=7737972;
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us-09-660-302e-1.rsp

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Score 25; DB 1; Le
Pred. No. 3.1e+02;
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146
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208 NEFIGVDS 215
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Chloroplast; Hypothe
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Best Local Similarity
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Q7M8B4;
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=VP-5482 / ATCC 29148;
STRAIN=VP-5482 / ATCC 29148;
MDDIANE=22550889; PubMed=12663928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
-!- FUNCTION: Catalyzes the formation of N(7)-methylguanine at position 46 (#7646) in tRNA (By similarity).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing N(7)-methylguanine.
-!- SIMILARITY: Belongs to the methyltransferase superfamily. TrmB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
tRNA (guanine-N(7)-)-methyltransferase (BC 2.1.1.33) (tRNA(m7G46)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02399; Methyltransf 4; 1.
ProDom; PD000288; Aldo/ket_red; 1.
Transferase; Methyltransferase; tRNA processing; Complete proteome.
SEQUENCE 280 AA; 32678 MW; 56F96C400D6CDEF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                            Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A. Orsat B., Spielmann A., Stutz B.; "Complete sequence of Euglena gracilis chloroplast DNA."; Nucleic Acids Res. 21:3537-3544(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 25; DB 1; Length 280; Pred. No. 3.1e+02; 4; Mismatches 0; Indels
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Last annotation update)
protein in FSBD intron 8 (ORF281A).
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NCBI_TaxID=3039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF 01057; -; 1.
InterPro; IPR001395; Aldo/ket red.
InterPro; IPR003358; Methyltransf_4.
InterPro; IPR000051; SAM_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93347989; PubMed=8346031;
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                                                                                                                         Bacteroides thetaiotaomicron.
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Hypothetical 33.0 kDa
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STRAIN=Z / UTEX 753;
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                                                                                  methyltransferase)
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Chloroplast.
                                                                                                                                                                                      NCBI_TaxID=818;
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Mayer F., Lederer H., Schuster S.C.;
T. Complete genome sequence and analysis of Wolinella succinogenes.";
T. Complete genome sequence and analysis of Wolinella succinogenes.";
T. Complete genome sequence and analysis of Wolinella succinogenes.";
T. Complete genome sequence and analysis of Wolinella succinogenes.";
T. Proc. Natl. Acad. Sci. U.S.A. 100:11699.11695(2003).
T. Frunction.
T. Proc. Natl. Acad. Sci. U.S.A. 100:11699(100:11695(2003)).
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable endonuclease IV (EC 3.1.21.2) (Endodeoxyribonuclease IV).
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Helicobacteraceae; Wolinella.
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PROSTER; FS00729; AP NUCLEASE F2 1; 1.
PROSTER; PS00731; AP NUCLEASE F2 2; 1.
PROSTER; PS00731; AP NUCLEASE F2 3; FALSE NEC.
Hydrolase; Nuclease; Endonuclease; DNA repair; Metal-binding; Zinc;
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281 AA; 33009 MW; 0B72FCE982FE320A CRC64;
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NCBI_TaxID=1502;
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P27897;
Clostridium
                                           STRAIN=13 /
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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase)
(SPDSY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                  STRAIN=Malish 7;
MEDLINE=2142074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPEE OR CPE0550.
Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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0
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                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 282;
                                                                                     Score 25; DB 1; Length 282;
Pred. No. 3.1e+02;
Mismatches 0; Indels
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50.0%; Pred. No. 3.18+02;
.ive 4; Mismatches 0; Indels
  ZINC 2 (BY SIMILARITY).
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ZINC 2 (BY SIMILARITY).
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ZINC 2 (BY SIMILARITY).
W, 9CRFGFF37D50BC09 CRC64;
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282 AA; 31331 MW; 8C9CDD6E47065445 CRC64;
                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein RC0079.
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                                                                                                   Pred. No. 3.1e
4; Mismatches
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                                                                      31169 MW;
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156 LEFIDKDG 163
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282 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                       Rickettsia conorii
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SPEE CLOPE
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01-AUG-1992 (Rel. 23, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
UTP--glucose-l-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase) (UDPGP) (Alpha-D-glucosyl-1-phosphate uridylyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                    flesh-eater.";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
-!- CATALYTIC ACTIVITY: S-adenosylmethioninamine + putrescine = 5'--
methylthicadenosine + spermidine.
-!- PATHWAY: Spermidine biosynthesis; fifth (last) step.
-!- PATHWAY: Belongs to the spermidine/spermine synthase family.
                                                 MEDLINE=21664373; PubMed=11792842; Shimizu T., Ohtani K., Harakawa H., Ohshima K., Yamashita A., Shimizu T., Ohtani K., Hirakawa H., Kuhara S., Hayashi H.; Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Profeobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Gluconacetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
MEDINE=92041556; PubMed=1938907;
MEDINE=92041556; PubMed=1938907;
MEDINE=92041556; PubMed=1938907;
MINCLEOTIVE SEQUENCE and expression analysis of the Acetobacter xylinum uridine diphosphoglucose pyrophosphorylase gene.";
J. Bacteriol. 173:7042-7045(1991).
-:- CATALYTIC ACTIVITY: UTP + alpha-D-glucose 1-phosphate = diphosphate + UDF-glucose.
-:- SIMILARITY: Belongs to the prokaryotic UDPGP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 1; Length 28.
Pred. No. 3.1e+02;
Pred. Op. 1ndels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; ARVOLLO;
HAMAP; MF 00198; -;
InterPro; IPR000051; SAM bind.
InterPro; IPR001045; Sprmine synthase.
InterPro; IPR001045; Sprmine synthase.
Pram, PR001564; Spermine Synth; 1.
TIGRPAM; TIGRO417; SpeE; 1.
PROSITE; PS01330; SPERMIDINE SYNTHASE; FALSE NEG.
Spermidine biosynthesis; Transferase; Complete proteome.
77 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 AA; 32992 MW; F546286DA257EB22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP003187; BAB80256.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 DEFIYHDM 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acetobacter xylinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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Les 4; Conserv
                                   Type A;
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SEQUENCE FROM N.A.
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32151 MW;

288 AA;

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "C SYMAINE_2022556; PubMed_alonfollogy and MEDLINE=2022556; PubMed_alonfollogy and MEDLINE=2022556; PubMed_alonfollogy and Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., A. Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T., A. Alee S.R., Morelli G., Basham D., Brown D., Chillingworth T., A. Jagels K., Leather S., Moule S., Mungall K., Quail M.A., A. Agaels K., Leather S., Moule S., Mungall K., Quail M.A., R. R. Asjandream M.A., Rutherford K.M., Simmonds M., Skelton J., R. R. Asjandream M.A., Rutherford K.M., Simmonds M., Skelton J., R. M. Mitchead S., Spratt B.G., Barrell B.G.; R. Complete DNA sequence of a serogroup A strain of Neisseria R. Mature 404:502-506(2000)

CC -! CATALYTIC ACTIVITY: dTTP + alpha-D-glucose I-phosphate = diphosphate + dTDP-glucose.

CC - CATALYTIC ACTIVITY: GTTP + alpha-D-glucose I-phosphate = CC - PATHWAY: RHAMNOSE BIOSYNTHESIS

CC -- PATHWAY: RHAMNOSE BIOSYNTHESIS

CC -- PATHWAY: PLIPOPOLYSACCHARIDE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24) (dTDP-glucose synthase)
(RFBA1 OR NRA0188) AND (RFBA2 OR NRA020S).
                                                                                                                                                                                                                                                                                                                                                    ·
0
                                                                                                                                                                                                                                                                                                     Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis (serogroup A).
Bacteria, Proteobacteria; Betaproteobacteria, Neisseriales,
                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 1; Length 28. 50.0%; Pred. No. 3.2e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                      6C809AFFBBA1791B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTR; H82014; H82014.
InterPro; IPR005907; GIP_thy_trans_1.
InterPro; IPR005907; GIP_thy_transferase.
Pfam; PF00483; NTP_transferase; 1.
TIGRFAMS; TIGR01207; rmlA; 1.
Lipopolysaccharide biosynthesis; Transferase; Kinase;
Nucleotidyltransferase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the glucose-1-phosphate thymidylyltransferase family.
                                                                                                                                                                         InterPro; IPR005835; NTP transferase.
Pfam; PF00483; NTP transferase; 1.
Transferase; Kinase; Nucleotidyltransferase.
SEQUENCE 284 AA; 30992 MW; 6C809AFFBBA17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Z2491 / Serogroup A / Serotype 4A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL162752; CAB83503.1; -. EMBL; AL162752; CAB83519.1; -.
                                                                                                                                      EMBL; M76548; AAA21888.1; -.
                                                                                                                                                                                                                                                                                                                 Best Local Similarity 50.0
Matches 4; Conservative
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120 REFIGNDP 127
                                                                                                                                                             PIR; A41382; A41382.
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                                                                                                                                                                                                                                                                                              Query Match
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  SX R R R R R S S S S S R R R R R R S S S S S R R R R R R R S S S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20175755; PubMed=10710307;
MEDLINE-20175755; PubMed=10710307;
Tertelln H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                         2.7.7.24) (dTDP-glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 287:1809-1815(2000).
-!- CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate =
diphosphate + dTDP-glucose.
-!- PATHWAY: RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN BIOSYNTHESIS
PATHWAY OF LIPPOPLYSACCHARIDE BIOSYNTHESIS.
-!- SIMILARITY: Belongs to the glucose-1-phosphate
thymidylyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=B1940 / Serogroup B;
MEDLINE=94293762; PubMed=8022265;
MEDLINE=94293762; PubMed=8022265;
MEDLINE=94293762; PubMed=802265;
Van Putten J.P.M., Ebeling O., Frosch M.;
"Contribution of genes from the capsule gene complex (cps) to lipoligosaccharide biosynthesis and serum resistance in Neisseria
                                                                                0;
                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glucose-l-phosphate thymidylyltransferase (EC 2.7.7.24) (dTE synthase) (dTDP-glucose pyrophosphorylase).
(RFBA1 OR NMB0062) AND (RFBA2 OR NMB0080).
Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria; Betaprotecobacteria, Neisseriales;
                                         Length 288;
                                                                              Indels
C818727C546F5E00 CRC64;
                                  100.0%; Score 25; DB 1; L
50.0%; Pred. No. 3.2e+02;
ive 4; Mismatches 0;
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InterPro; IPR005835; NTP_transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L09189; AAC37050.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Microbiol. 11:885-896(1994).
                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
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EMBL, AE002367; AAF40544.1; --
PIR, B81240; B81240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseriaceae, Neisseria.
NCBI_TaxID=491;
                                                                          4; Conservative
                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                 8
                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                            1 XEFIXXDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         meningitidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; NMB0080;
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RFBA NEIMB
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ARY2 MOUSE
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ARY2 MOUSE
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STRAIN-UAIS9 / ATCC 700610 / Serotype C;
STRAIN-UAIS9 / ATCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UAIS9, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24) (dTDP-glucose synthase) (dTDP-glucose pyrophosphorylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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-!- CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate diphosphate + dTMP-glucose.
-!- PATHWAY: dTDP-L-rhamnose biosynthesis.
-!- PATHWAY: Belongs to the glucose-1-phosphate thymidylyltransferase family.
                                                                                                                                                                                                                                                                                                                                   Score 25; DB 1; Length 288; Pred. No. 3.2e+02; 4; Mismatches 0; Indels
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Tsukioka Y., Yamashita Y., Nakano Y., Oho T., Koga T.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5563650C07C00987 CRC64;
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                                                                                                                                                                                                                                                    8A65B50B531F2907 CRC64;
Pfam; PF00485; with the program of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the propert
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InterPro; IPR005907; GIP thy trans.1.
InterPro; IPR005895; NTP transferase.
Pfam; PF00483; NTP transferase.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
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198 198 T
288 AA; 32161 MW;
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50.0%; E
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TIGREAMs; TIGR0120\overline{	ilde{7}}; rmlA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D78182; BAA11247.1;
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 EEFIGNDN 101
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1309;
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P95778;
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CONFLICT
SEQUENCE
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RMLA_STRMU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAL.1 and Nat-2 gene products.";

Mol. Pharmacol. 42:265-272(1992).

-!- FUNCTION: Participates in the detoxification of a plethora of hydrazine and arylamine drugs. 2-aminofluorene and p-aminobenzoic acid (PABA) are preferred substrates for NAT-2. Less activity with anisidine and barely detectable with SMZ.

-!- CATALYTIC ACTIVITY: Acetyl-CoA + an arylamine = CoA + an N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- POLYMORPHISM: There are two forms of NAT2: a rapid/stable isoform (Asn-99) and a slow/unstable isoform (Ile-99).
-!- SIMILARITY: Belongs to the arylamine N-acetyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92382565; PubMed=1513324; Martell K.J., Levy G.N., Weber W.W.; Martell K.J., Levy G.N., Weber W.W.; "Cloned mouse N-acetyltransferases: enzymatic properties of expressed
                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
Arylamine N-acetyltransferase 2 (EC 2.3.1.5) (Arylamide acetylase 2)
(N-acetyltransferase type 2) (NAT-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ಗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martell K.J., Vatsis K.P., Weber W.W.; "Molecular genetic basis of rapid and slow acetylation in mice."; Mol. Pharmacol. 40:218-227(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=94379961; PubMed=7545952;
Kelly S.L., Sim E.,
"Arylamine N-acetyltransferase in Balb/c mice: identification of novel mouse isoenzyme by cloning and expression in vitro.";
Biochem. J. 302:347-353(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C3H/HeJ; TISSUE=Heart;
Hein D.W., Doll M.A.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                        290 AA.
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MGD; MGI:109201; Nat2.
InterPro; IPR004081; AANacetyltransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6, and A/J;
MEDLINE=91342604; PubMed=1875909;
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                                                                                                                                                                                                                                        STANDARD;
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94 EEFIGDDH 101
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   1 XEFIXXDX
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139 TEFIGNDD 146

RESULT 78

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InterPro; IPR001447; Acetyltransf2.
Pfam; PF00797; Acetyltransf2; 1.
PRINTS; PR01543; ANATRNSFRASE.
ProDom; PD002783; Acetyltransf2; 1.
Transferase; Acyltransferase; Multigene family; Polymorphism.
Acyltransferase; By SIMILARITY.
Acyltransferase; Now, unstable of the state of t
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                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                  704E000DE48CE557 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                          100.0%; Score 25; DB 1;
50.0%; Pred. No. 3.2e+02;
tive 4; Mismatches 0;
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable GTPase engC (RC 3.6.1.-).
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GTP (PROBABLE).
GTP (PROBABLE).
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TIGRPAMs; TIGR00157; TIGR00157; 1.
PROSITE; PS50936; ENGC GTPASE; 1.
Hydrolase; GTP-binding.
                                                                                                                                                                                                             290 AA; 33701 MW;
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291 AA; 33890 MW;
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HAMAP; MF_01820; -; 1.
InterPro; IPR004881; DUF258.
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Best Local Similarity 50.00,
hnc 4; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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173 QEFINSDL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lancet 359:1819-1827(2002).
-!- FUNCTION: Unusual circulary permuted GTPase that catalyzes rapid hydrolysis of GTP with a slow catalytic turnover (By similarity).
-!- SUBUNIT: Monomer (Probable).
-!- SIMILARITY: Contains 1 engC GTPase domain.
                                                                                                                                                                                                                                                  PETRAIN-MULSO (ATC. 700699, and N315; MEDLINE-21311952; PubMed=11418146; Kurdad M., Otha T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mutatani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Whiba S., Wabusaki J., Mulatori M., Ogasawara G., Raito II., Firamatsu K.; Wattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Shiba W., Manani S., Wabusaki J., Kanen Sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STEAIN=MW2;
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagai Y., Iwama N., Asano K., Nalmı 1., hurowa...,
Yamamoto K., Hiramatsu K.,
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 291;
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                                15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Probable GTPase engc (EC 3.6.1.-).
ENGC OR SAV1221 OR SA1064 OR MW1104.
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain M35), and
Staphylococcus aureus (strain M35), and
Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TAXID=158878, 158879, 196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; 50.0%; Pred. No. 3.2e+02;
     291 AA.
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EMBL; AP003133; BAB42316.1; --
EMBL; AP004826; BAB94869.1; --
PIR; H89894; H89894.
HAMAP; MF 01820; --; 1.
InterPro; IPR004881; DUF258.
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   STANDARD;
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164
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291 AA;
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Best Local Similarity
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Q99UP7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jiang X.-M., Neal B., Santiago F., Lee S.J., Romana L.K., Reeves P.R.; "Structure and sequence of the rfb (O antigen) gene cluster of Salmonella serovar typhimurium (strain LT2)."; Mol. Microbiol. 5:695-713(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:852-856(2001)

-!- CATALYTIC ACTIVITY: a(TTP + alpha-D-glucose 1-phosphate = diphosphate + dTDP-glucose.

-!- PATHWAY: DTDP-L-RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.

-!- SIMILARITY: Belongs to the glucose-1-phosphate thymidylyltransferase family.
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Lipopolysaccharide biosynthesis; Transferase; Kinase;
Nucleotidyltransferase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 1; L. 50.0%; Pred. No. 3.3e+02; ive 4; Mismatches 0;
                                                                           01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-EB-2003 (Rel. 41, Last annotation update)
Succese-1-phosphate thymidylyltransferase (EC synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ā
                   292 A.A.
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InterPro, IPR005835; NTP transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00483; NTP transferase; 1.
TIGRFAMS; TIGR01207; rmlA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91260454; PubMed=1710759;
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292 AA; 32453 MW; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X56793; CAA40117.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE008792; AAL20999.1;
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                          STANDARD;
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StyGene; SG10449; rfbA.
                                                                                                                                                                                                                                                                                 Salmonella typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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RFBA SHIFL
ID RFBA SHIFL ST
AC P37779; Q54164;
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                          SALTY
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                          RFBA SP
P26393
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MEDLINE=93273708; PubMed=7684736;
Liu D., Haase A.M., Lindqvist L., Lindberg A.A., Reeves P.R.;
"Glycosyl transferases of O-antigen biosynthesis in Salmonella
enterica: identification and characterization of transferase genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang L., Romana L.K., Reeves P.R.; "Molecular analysis of a Salmonella enterica group El rfb gene cluster: O antigen and the genetic basis of the major polymorphism."; Genetics 130:429-443(1992).
                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1997 (Rel. 35, Last annotation update)
Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24) (dTDP-glucose synthase) (dTDP-glucose pyrophosphorylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=58712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     groups B, C2, and E1.";
J. Bacteriol. 175:3408-3413(1993).
-!- CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate = diphosphate + dTDP-glucose Blucose.
-!- PATHWAY: DTDP-L-FHAMNOSE BLOSYNTHESIS WITHIN THE O ANTIGEN BLOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BLOSYNTHESIS.
-!- SIMILARITY: Belongs to the glucose-1-phosphate
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Pred. No. 3.3e+02;
4; Mismatches 0; Indels
   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipopolysaccharide biosynthesis, Transferase, Kinase, Nucleotidyltransferase.
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0
      Mismatches
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InterPro; IPR005835; NTP transferase.
Pfam; PF00433; NTP transferase; 1.
TIGRFAMS; TIGR01207; rm18, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=M32 / Group E1;
MEDLINE=92201631; PubMed=1372579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thymidylyltransferase family.
      4;
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      Conservative
                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                         139 TEFIGNDD 146
                                                                 1 XEFIXXDX 8
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Matches 4; Conserv
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P55254;
      4;
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Gaps

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Length 292; Indels ó

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  01-OCT-1994 (Rel. 30, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24) (dTDP-glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=201 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of Shigella flexmeri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                           Macpherson D.F., Manning P.A., Morona R., "Characterization of the dTDP-rhamnose biosynthetic genes encoded in the rfb locus of Shigella flexmeri."; Mol. Microbiol. 11:81-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence of the rhamnose biosynthetic operon of Shigella flexneri 2a and role of lipopolysaccharide in virulence.";
J. Bacteriol. 176:2362-2373(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diphosphate + drop-glucose.
-!- PATHWAY: RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.
-!- SIMILARITY: Belongs to the glucose-l-phosphate thymidylyltransferase family.
                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIRS_25590747 ATCC 700930 / Serotype 2a;

MEDLINE=2259074; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Wei J., Goldberg M.S., Burland V., Venkatesan M.M., Deng W.,
Wei J., Bornier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
Mau B., Perra N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blather F.R.;
Complete genome sequence and comparative genomics of Shigella
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-YSH6200 / Serotype 2a;
MEDLINE=94209238; PubMed=8157605;
Rajakumar K., Jost B.H., Sasakawa C., Okada N., Yoshikawa M.,
Adler B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  flexmeri serotype 2å strain 2457π.",
Infect. Immun. 71:2775-2786(2003).
-!- CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate =
                                                                                     synthase) (dTDP-glucose pyrophosphorylase). RFBA OR SF2102 OR S2225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, S41536, S41536.
Interpro, IPR005907, G1P thy trans l.
Interpro, IPR005935, NP transferase.
Pfam, PF00483, NTP_transferase, l.
                                                                                                                                                                                                                                                      STRAIN=PE577 / Serotype 2a;
MEDLINE=94224146; PubMed=8170390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE015225; AAN43641.1; -. EMBL; AE016985; AAP17470.1; -.
                                                                                                                                                                   Enterobacteriaceae, Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X71970; CAA50769.1; -.
EMBL; L14842; AAA53681.1; -.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                            Shigella flexneri
                                                                                                                                                                                      NCBI_TaxID=623;
                                                                                   synthase)
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STRAIN=K12 / WG1;
MEDLINE=94292435; PubMed=7517391;
Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,
Redmond J.W., Lindquist L., Reeves P.R.;
"Structure of the O antigen of Escherichia coli K-12 and the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.7.7.24) (dTDP-glucose
                                                                                                                                                                                                                                 Gaps
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MEDLINE=9745617, PubMed=9278503;
MEDLINE=9745617, PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SERVIN-EX.2;
MEDLINE-87251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T., Aiba H., Raba T., Fujita K., Mikitagawa M., Kitagawa M., Kitagawa M., Mixobuchi K., Mori T., Morobuchi K., Mori H., Mori T., Motomura X., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundarama S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T., "A 460-kb DNA sequence of the Escherichia coli K-12 genome
                                                                                                                                                                                                                               0;
                                                                                                                                                                                        100.0%; Score 25; DB 1; Length 292; 50.0%; Pred. No. 3.3e+02; Live 4; Mismatches 0; Indels
            Lipopolysaccharide biosynthesis; Transferase; Kinase; Nucleotidyltransferase; Complete proteome.

Nucleotidyltransferase; Complete proteome.

CONFLICT 157 A -> P (IN REF. 1).

CONFLICT 215 15 MISSING (IN REF. 1).

CONFLICT 224 224 W -> C (IN REF. 1).

CONFLICT 224 233 GTHQSL -> DTSKP (IN REF. 1).

CONFLICT 243 245 IEE -> NED (IN REF. 1).

SEQUENCE 292 AA; 32487 MW; E54F6199E036IAF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stevenson G.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
TIGR01207; rmlA; 1.
                                                                                                                                                                                                                                                                                                                                                                           TEAL ECOLI STANDARD; PRT; 293 AA. P37744; P780B1; 201-0CT-1994 (Rel. 30, Created) 01-0CT-1997 (Rel. 35, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) glucose-1-phosphate thymidylyltransferase (EC. STATABASE) (dTDP-glucose pyrophosphorylase). RFBA OR RMLA OR B2039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               its rfb gene cluster.";
Bacteriol. 176:4144-4156(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [5]
SEQUENCE OF 247-293 FROM N.A.
                                                                                                                                                                                                                              Conservative
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97 EEFIGGDD 104
                                                                                                                                                                                                                                                            1 XEFIXXDX 8
                                                                                                                                                                                                        Best_Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISION TO 288.
STRAIN=K12 / WG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562;
                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                              RESULT 82
DR
ETT FT
SO FT
SO FT
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Biochem. 230:906-913(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SETALM=AV19 / DSM 6324 / JCM 9639;
MEDLINE=AV19 / DSM 6324 / JCM 9639;
MEDLINE=95324581; PubMed=7601152;
Shima S., Weiss D.S., Thauer R.K.;
"Formylmethanofuran:terrahydromethanopterin formyltransferase (Ftr)
from the hyperthermophilic Methanopyrus kandleri. Cloning, sequencing
and functional expression of the ftr gene and one-step purification
of the enzyme overproduced in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
Methanopyrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                             Yao Z., Valvano M.A.; "Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (rfb) of Eschericia coli K-12 W3110: identification of genes that confer group 6 specificity to Shigella flexneri serotypes Y and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Formylmechanofuran-tetrahydromethanopterin formyltransferase (EC 2.3.1.101) (H4MPT formyltransferase).
                                                                                          J. Bacteriol. 176:4133-4143(1994).
-!- CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate = diphosphate + dTDP-glucose Biosynthesis WITHIN THE O ANTIGNIES PATHWAY: DTDP-L-RIAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGNIES BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 25; DB 1; Length 293; Pred. No. 3.3e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Libopolysaccharide biosynthesis; Transferase; Kinase; Nuclectidyltransferase; Complete proteone; 3D-structure. CONFLICT 247, Q -> P (IN REF. 5). SEQUENCE 293 Aa, 32693 MW, BA895362DICSCA55 CRC64;
                                                                                                                                                        -!- SIMILARITY: Belongs to the glucose-1-phosphate thymidylyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 AA
                                                                                                                                                                                                                                                                                                        EMBL; AE000294; AAC75100.1; --
EMBL; D90841; BAA15881.1; --
EMBL; D90842; BAA15881.1; --
EMBL; U03041; BAA15893.1; --
PIR; F64969; F64969.
PDB; 1H57; 08-MAY-02.
SWISS-2DPAGB; P3744; COLI.
ECOGENE; EG11978; rfbA.
InterPor; IPR005897; GTP thy trans 1.
InterPor; IPR005835; NTP transferase.
Pfam; PF00483; NTP transferase.
TIGRPAMS; TIGR01077; rmlA; 1.
      STRAIN=K12 / W3110;
MEDLINE=94292434; PubMed=7517390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                                                                                                                                                                                                                   EMBL; U09876; AAB88400.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanopyrus kandleri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | | | :: | :
97 EEFIGGDD 104
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Best Local Similarity
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FTR OR MK0116
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Q49610;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- FUNCTION: Catalyzes the reversible transfer of a formyl group from formylmethanofuran (formyl-MFR) to tetrahydromethanopterin (H(4)MPT) so as to produce 5-formyl tetrahydromethanopterin formyl-H(4)MPT) and methanofuran (MFR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Salt dependence, kinetic properties and catalytic mechanism of N-formylmethanofuran:tetrahydromethanopterin formyltransferase from the extreme thermophile Methanopyrus kandleri.";

Bur. J. Blochem. 210:971-981(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanogenesis; One-carbon metabolism; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97341227; PubMed-9195883; Brima S.; Merckel M., Thauer R., Shima S.; Forwylmethanofuran: tetrahydromethanopterin formyltransferase from Methanopyrus kandleri - new insights into salt-dependence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: Methanogenesis from carbon dioxide; second step.
-!- SUBUNIT: Homoterramer composed of two dimers. Dimerization is sufficient for enzyme activity, but tetramerization is required for high thermostability.
SEQUENCE FROM N.A.

STRAIN-AV19 / DSM 6324 / JCM 9639;

MEDLINE=21927647; PubMed=11930014;

Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

Slesarev A.I., Mezhevaya K.V., Belova G.I., Aravind L.,

Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,

Malykh A.G., Koonim E.V., Kozyavkin S.A.,

"The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A mutation affecting the association equilibrium of formyltransferase from the hyperthermophilic Methanopyrus kandleri and its influence on the enzyme's activity and thermostability."; Eur. J. Biochem. 267:6619-6623(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tetrahydromethanopterin = methanofuran + 5-formyl-5,6,7,8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tetrahydromethanopterin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20507566; PubMed=11054114;
Shima S., Thauer R.K., Ermler U., Durchschlag H., Tziatzios
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Breitung J., Borner G., Scholz S., Linder D., Stetter K.O., Thauer R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the FTR family.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-49, AND CHARACTERIZATION.
MEDLINE=93130924; PubMed=1483480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT, AND MUTAGENESIS OF ARG-261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF 00579; -; 1.
InterPro; TRR002770; FTR.
Pfam; PP01913; FTR. 1.
Pfam; PP02741; FTR C; 1.
PIRSF; PIRSF006414; FTR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thermostability.";
Structure 5:635-646(1997)
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PDB; 1FTR; 25-NOV-98.
HAMAP; MF_00579; -; 1
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CSTRAINAATCC 824 DSM 792 / VKM B-1787;

XM WEDLINE=21359325; PubMed=11466286;

XM WEDLINE=21359325; PubMed=11466286;

XM WEDLINE=21359325; PubMed=11466286;

XM WEDLINE=21359325; PubMed=11466286;

XM Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

XM Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

XM Bennett G.N., Koonin B.V., Smith D.R.;

XM Genome sequence and comparative analysis of the solvent-producing

XM Genome sequence and comparative analysis of the solvent-producing

XM Genome sequence and comparative analysis of the solvent-producing

XM Genome sequence and comparative analysis of the solvent-producing

XM Genome sequence and comparative analysis of the solvent-producing

XM Genome sequence and comparative and proteins from

XM Introversible aggregation. Plays an important role in the bacterial

XM Gefense system toward oxidative stress (By similarity).

YM Gefense system toward oxidative two disulfide bonds are formed

Introlving the reactive cysteines and the protein is inactive (By

Similarity).
                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
       Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriophage HPI.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Esposito D., Fitzmarrice W.P., Benjamin R.C., Goodman S.D., Waldman A.S., Scocca J.J.,
"The complete nucleotide sequence of bacteriophage HPI DNA.",
Nucleic Acids Res. 24:2360-2386(1996).
-!- SIMILARITY: STRONG, TO PHAGE P2 PROTEIN O.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PI; Zinc; Complete proteome.
REDOX-ACTIVE (BY SIMILARITY)
REDOX-ACTIVE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4E3B64521077316D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 25; DB 1; L
Pred. No. 3.3e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01430; HSP33; 1.
ProDom; PD248154; Hsp33; 1.
Chaperone; Redox-active center; Zinc; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPO_BPHP1 STANDARD; PRT; 298 AA. P51719; PCT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last annotation update) Probable capsid scaffolding protein (ORF17).
                                                                                                                                                                                                                                                  similarity).
SIMILARITY: Belongs to the HSP33 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96279738; PubMed=8710508;
                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE007737; AAK80326.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 AA; 32033 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
50.0%; P
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HAMAP, MF 00117; -; 1.
InterPro; IPR000397; Hsp33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
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217 LEFIFEDM 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                   SEQUENCE FROM N.A.
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                           NCBI_TaxID=1488;
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DISULFID
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VPO_BPHP1
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           R->E: WEAKENS DIMER-DIMER ASSOCIATION.
THERMOLABILE.
H -> D (IN REF. 3).
W -> K (IN REF. 3).
E -> K (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 25; DB 1; Length 296;
Pred. No. 3.3e+02;
4; Mismatches 0; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
33 kDa chaperonin (Heat shock protein 33 homolog) (HSP33).
HSLO OR CAC2370.
Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31661 MW; DDE02D3E7D98FC86 CRC64;
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  Complete proteome
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                                                                                                                                                                                                                      102
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150 GEFIVEDS 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity
 3D-structure;
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Q97GJ6;
                                          CONFLICT
CONFLICT
STRAND
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HSLO_CLOAB
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Length 297;

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Matches
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                                                                                                                                                                ; Score 25; DB 1; Length 298; Pred. No. 3.3e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al protein; Complete proteome.
298 AA; 34256 MW; EBD06E78B3D3F8EF CRC64;
                                                                                                                                            298 AA; 33702 MW; 6D2841468D700C1F CRC64;
                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AQ_2144.
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                                                                                                                                                                                                                                                                                                    298 AA
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MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000775; AAC07871.1; -. PIR; H70483; H70483; H70484 Hypothetical protein; Complete SEQUENCE 298 AA; 34256 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
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16-OCT-2001 (Rel. 40, Last sem
                                                                                                                                                                    100.0%;
                                                                                                           EMBL; U24159; AAB09202.1; -. PIR; S69523; S69523.
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                                                                                                                                                                                             4; Conservative
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                                                                                                                                                                                                                                                                                                       STANDARD;
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227 EEFILEDF 234
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142 GEFIKVDF 149
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Best Local Similarity
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Aquifex aeolicus.
                                                                                                                                  Capsid assembly SEQUENCE 298
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                        Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
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"Molecular basis of symbiosis between Rhizobium and legumes.";
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pantothenate kinase (BC 2.7.1.33) (Pantothenic acid kinase).
                                                                                                                                               Plasmid sym pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 1; Length 30 50.0%; Pred. No. 3.46+02; cive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000078; AAB91701.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 305 AA; 34141 MW; 331117881829F351 CRC64;
01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) Hypothetical 34.1 kDa protein Y41F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 AA
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                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
                                                                                                                   Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: None obvious.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||::|:
113 IEFIRGDI 120
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les 4; Conserva
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STRAIN=2603 V/R / Serotype V;
STRAIN=2603 V/R / Serotype V;
STRAIN=2222988 pubbhed=12200547;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Wasdoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay V.F., Madupu K., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Riacobini B.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphopantothenate.
-!- PATHWAY: Coenzyme A (COA) biosynthesis; first step.
-!- SUBCELDULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the prokaryotic pantothenate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=NEM316 / Serotype III;
STRAIN=NEM316 / Serotype III;
STRAIN=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek_T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence and comparative genomic analysis of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         emerging human pathogen, serotype V Streptococcus agalactiae.",
Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002)
-!- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
                                                                                                                                                                                                                                                                         ..
O
                                                                                                                                                                                                                               Score 25; DB 1; Length 306;
Pred. No. 3.4e+02;
; Mismatches 0; Indels
            EMBL; AE006374; AAK05542.1; -.
PIR; D86805, D86805.
HAMAP; MF 00215; -.; 1.
HAMAP; MF 00215; -.; 1.
InterPro; IPR04566; Pank bact.
InterPro; IPR060693; PRK_URK.
Pfam; PF00485; PRK; 1.
PIRSF: PIRSF000545; Pantothenate_kin; 1.
Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                   QBESPZ; QBDZZI;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Pantothenate kinase (EC 2.7.1.33) (Pantothenic acid kinase)
COAA OR GBS0939 OR SAG0951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus agaiactiae (serotype v).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                              ATP (POTENTIAL).
: 87241BDFC3FC9DB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus agalactiae (serotype III), and Streptococcus agalactiae (serotype V).
                                                                                                                                                                                                                                               Pred. No. 3.4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
                                                                                                                                                                                           SEQUENCE 306 AA; 35992 MW;
                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                               50.08;
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2 NEFINFDE 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91194547; PubMed=1901616;

Perego M., Higgins C.F., Pearce S.R., Gallagher M.P., Hoch J.A.;

"The oligopeptide transport system of Bacillus subtilis plays a role in the initiation of sporulation.";

Mol. Microbiol. 5:173-185(1991).
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InterPro; IPR004566; Pank bact.
InterPro; IPR006083; PRK ÜRK.
Pfam; PF00485; PRK; I.
PIRSF; PIRSF000545; Pantothenate kin; 1.
Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 1; Length sow
Pred. No. 3.4e+02;
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01FF015134D76D34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P2413_77; 031599; P23366; 01-MAR-1992 (Rel. 21, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) 01igopeptide transport ATP-binding protein oppF. OPPF OR SPOOKE OR BSU11470.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                               or send an email to license@isb-sib.ch)
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                                                                                                     EMBL; AL766848; CAD46598.1; -.
                                                                                                                                         EMBL; AE014235; AAM99835.1; -.
SagaList; gbs0939; -.
TIGR; SAG0951; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
NP BIND 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1423;
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OPPF_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interro.,
A interpro; IRRUULL...
B fine Pro; IRRUULL...
IN Pfam; PF00056; ldh, 1.
IN PROBG6; ldh C; 1.
IN PROBG6; ldh C; 1.
IN PROBG6; LiDHDRGMASE.

DR PROBTIE; PS00068; MAD; FALSE NEG.

DR PROBGE STREE TRICARDOXYLIC acid cycle; NAD; 3D-structure.

FW Oxidoreductase; Tricarboxylic acid cycle; NAD; 3D-structure.

FT ACT SITE 148 SUBSTRAITY).
FROTON-RELAY (BY SIMILARITY).
FROTON-RELAY (BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                Rolstad A.K., Howland E., Sirevag R.;

Rolstad A.K., Howland E., Sirevag R.;

Malate dehydrogenase from the thermophilic green bacterium chloroflexus aurantiacus: purification, molecular weight, amino acid composition, and partial amino acid sequence.";

J. Bacteriol. 170:2947-2953(1988).

-!- CATALYTIC ACITIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.

-!- CATALYTIC ACITIVITY: (S)-malate + NAD(+) = toxaloacetate + NADH.

AT TEMPERATURES LOWER HAAN 55 DEGREES CELSIUS (INACTIVE FORMS).

-!- SIMILARITY: Belongs to the LDH family. MDH subfamily.
                           STRAIN=J-10-f1;
MEDLINE=96241868; PubMed=8661927;
Synstad B., Emmerhoff O., Sirrevag R.;
"Malate dehydrogenase from the green gliding bacterium Chloroflexus
aurantiacus is phylogenetically related to lactic dehydrogenases.";
Arch. Microbiol. 165:346-353(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=92250599; PubMed=1339458;
Schlaepfer_D.D., Fisher D.A., Brandt M.E., Bode H.R., Jones J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 25; DB 1; Length 30
Pred. No. 3.5e+02;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Annexin B12 (Annexin XII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 A.A.
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                                                                                                                                                                                                                                                                                                            STRAIN=J-10-f1;
MEDLINE=88257004; PubMed=3133356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X89038; CAA61436.1; -. PDB, 1GUY, 13-UNN-02.
INTERPRO; IPR001557; L.LDH.
INTERPRO; IPR001257; MGh.AS.
INTERPRO; IPR001252; MGh.AS.
INTERPRO; IPR0002057; NAD_BS.
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194 SEFIAPDR 201
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          SEQUENCE FROM N.A.
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Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Oglwara A., Oudega B., Park S.H.,
Parts V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Resecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Sadale Y.,
Rivolta C., Rocha E., Roche B., Roche B., Society M., Sadale Y.,
A sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
A sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
Sorokin A., Tacconi E., Takadashi H., Takemau K.,
Takeuchi M., Tamakoshi A., Tanaka T., Tareparu K.,
A Takeuchi M., Tamakoshi A., Tanaka T., Tareparu K.,
A Tosato V., Uchiyama S., Vandelor M., Wannier F., Vassarotti A.,
Vari A., Wambutt R., Wedler E., Wedler F., Weitzenegger T.,
Winters P., Mipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
A Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
T. "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroflexi; Chloroflexales; Chloroflexaceae; Chloroflexus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997).

-i- FUNCTION: Component of the oligopeptide permease, a binding protein-dependent transport system. Necessary for genetic competence but not sporulation. Probably responsible for energy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSO0211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
Competence; Peptide transport; Transport; Membrane; ATP-binding;
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308 AA; 35104 MW, F17DE0016AA3B4ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coupling to the transport system.
SUBCELLUIAR LOCATION: Membrane-associated.
SIMILARITY: Belongs to the ABC transporter family.
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Last annotation update)
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EMBL; M57689; AAA25692.1; -.
EMBL; M7689; AAA62693.1; ALT_INIT.
EMBL; Z99110; CAB313004.1; ALT_INIT.
PIR; E33447; E38447.
Subtilist; B010775; OppF.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
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ProDom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; 1.
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01-NOV-1997 (Rel. 35, Last seq
10-OCT-2003 (Rel. 42, Last anno
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NCBI_TaxID=1108;
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                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF MUTANT LYS-105.
MEDLINE=20170873; PubMed=10704197;
Cartailler J.P., Haigler H.T., Luecke H.;
"Annexin XII E105K Crystal structure: identification of a pH-dependent switch for mutant hexamerization.";
Biochemistry 39:2475-2483(2000).
-! SUBLUIT: Homohexamer.
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.

PIT: Phosphorylated in vitro on serine(s) and threonine(s) by PKC. SIMILARITY: Belongs to the annexin family.

SIMILARITY: Contains 4 annexin repeats.

DATABASE: NAME-Annexin 12 home page from Luecke's group;

WWW="http://anx12.bio.uci.edu/~hudel/anx12/".
Characterization, cDNA cloning, and protein kinase C phosphorylation
                                                                                X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=96085034; PubMed=7477411;
Luecke H., Chang B.T., Maillard W.S., Schlaepfer D.D., Haigler H.T.,
"Crystal structure of the annexin XII hexamer and implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANNEXIN 4.
PHOSPHORYLATION (BY PKC) (POTENTIAL)
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PROSITE; PS00223; ANNEXIN; 3.
Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
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ANNEXIN 2.
ANNEXIN 3.
                          annexin XII.";
Biol. Chem. 267:9529-9539(1992).
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PDB; 1DM5; 20-MAR-00.
InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
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ProDom; PD000143; Annexin; 4.
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                                                                                                                                                                                      Nature 378:512-515(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {RNA}(N).
--- SUBUNIT: Homodimer. The RNAP catalytic core consists of 2 alpha, 1
beta, 1 beta' and 1 omega subunit (By similarity).
--- DOMAIN: The N-tendinal domain is essential for RNAP assembly and
basal transcription, whereas the C-terminal domain is involved in
interaction with transcriptional regulators and with upstream
promoter elements (By similarity).
--- SIMILARITY: Belongs to the RNA polymerase alpha chain family.
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALPHA N-TERMINAL DOMAIN (ALPHA-NTD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
ALPHA C-TERMINAL DOMAIN (ALPHA-CTD)
                                                                                                                                .,
                                                                                      100.0%; Score 25; DB 1; Length 316; 50.0%; Pred. No. 3.6e+02; Live 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00662; RPOLD; 1. _____Transferase; Transcription; DNA-directed RNA polymerase;
                                                      35108 MW; 10599869CBA853EC CRC64;
                                                                                                                                                                                                                                                                                              PRT; 317 AA.
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HAMAP, MF 00059; -; 1.

InterPro; IPR0019025; RBP11-like RNApo.

InterPro; IPR001700; RNA polA bac_org.

Pfam; PF01000; RNA polA bac; 1.

Pfam; PF03118; RNA polA cTD; 1.

ProDom; PD01179; RNA polA corg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000672; AAC06440.1; -. PIR; H70306; H70306.
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                            STANDARD;
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279 2
294 3
304 3
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                                                                                    Query Match
Best Local Similarity
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Aquifex aeolicus.
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(COVALENT) (BY SIMILARITY).
(HEME AXIAL LIGAND) (BY SIMILARITY)
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Kingyoku;
Wakasugi T., Nishikawa A., Yamada K., Sugiura M.;
"Complete nuclectide sequence of the chloroplast genome from a fern,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein (By similarity).
--- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane. Membrane-anchored (By similarity).
--- SIMILARITY: Belongs to the cytochrome c family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BMBL; ArUncoc,
HAMAP; MF_00610; -: 1.
InterPro; IPR002325; Apocyt_F.
InterPro; IPR00345; CytC_heme_BS.
Pfam; PR0133; Apocytochr_F C; 1.
PR104133; Apocytochr_F C; 1.
PR01515; PR00610; CYTOCHROME; C; 1.
Blectron transport; Heme; Chloroplast; Thylakoid; Photosynthesis; Photosystem I; Photosystem II; Transmembrane; Signal.
SIGNAL 35 APOCYTOCHROME F.

APOCYTOCHROME F.
                                                                                                                                                                                                                                                                                                                        Chloroplast.
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Moniliformopses; Psilotophyta; Psilotales; Psilotaceae; Psilotum.
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IRON (HEME AXIAL LIGAND) (VIA AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Interacts with plastocyanin and Rieske iron-sulfur
                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 25; DB 1; Length 321; Pred. No. 3.6e+02; 4; Mismatches 0; Indels
                                      Score 25; DB 1; Length 317;
Pred. No. 3.6e+02;
; Mismatches 0; Indels
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          317 AA; 35768 MW; BC6EEB9015163335 CRC64;
                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
(BY SIMILARITY)
                                                      Pred. No. 3.6e
4; Mismatches
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                                                         50.0%;
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CYF_PSINU
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MEDLINE=94191542; PubMed=8142907; Padlan E.A., Helm B.A.; modeling of the lectin-homology domains of the human and murine lowaffinity Fc epsilon receptor (Fc epsilon RII/CD23)."; Receptor 3:325-341(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87218454; PubMed=3034567;
Luedin C., Hofstetter H., Sarfati M., Levy C.A., Suter U., Alaimo D.,
Kilchherr E., Frost H., Delespesse G.;
"Cloning and expression of the cDNA coding for a human lymphocyte IgE
                                  01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2014 (Rel. 43, Last annotation update)
16-MAR finity immunoglobulin epsilon FC receptor (Lymphocyte IgE
receptor) (FC-epsilon-RII) (CD23) (BLAST-2) (Immunoglobulin E-binding
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=87051737; PubMed=2877743;
Kikttani H., Inui S., Sato R., Barsumian E.L., Owaki H.,
Yamasaki K., Kaisho T., Uchibayashi N., Hardy R.R., Hirano T.,
Tsunasawa S., Sakiyama F., Suemura M., Kishimoto T.;
"Molecular structure of human lymphocyte receptor for immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yokota A., Kikutani H., Tanaka T., Sato R., Barsumian E.L., Suemura M., Kishimoto T., "Two species of human Fc epsilon receptor II (Fc epsilon RII/CD23): tissue-specific and IL-4-specific regulation of gene expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE, AND DISULFIDE BONDS.
MEDLINE=93038513; PubMed=1417742;
MEDLINE=93038513; PubMed=1417742;
Jansen K. Turcatti G., Graber P., Pochon S., Regamey P.-O.,
Jansen K.U., Magnenat E., Aubonney N., Bonnefoy J.-Y.;
"Partial characterization of natural and recombinant human soluble
                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                        Human lymphocyte Fc receptor for IgE: sequence homology of its
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-87118255; PubMed-2949326;
Ikuta K., Takami M., Kim C.W., Honjo T., Miyoshi T., Tagaya Y.,
                                                                                                                                                                                                                                                                                                                                             cloned cDNA with animal lectins.";
Proc. Natl. Acad. Sci. U.S.A. 84:819-823(1987).
 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [6]
3D-STRUCTURE MODELING OF LECTIN DOMAIN.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89028672; PubMed=2972386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3D-STRUCTURE MODELING OF 173-285.
MEDLINE=96276216; PubMed=8745401;
Bajorath J., Aruffo A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. J. 286:819-824(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 6:109-114(1987).
 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                               Kawabe T., Yodoi J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI_TaxID=9606;
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us-09-660-302e-1.rsp

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MEDLINE=95183147; PubMed=7877695;
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MEDLINE=95249601; PubMed=7732022;
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         230 GÉFIWVĎG 237
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STRAIN=S288C;
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                                                                                                                                                                PTM: N- and O-glycosylated.

MISCELLANBOUS: There are two kinds of Fc receptors for 1gE, which differ in both structure and function: high affinity receptors on basophils and mast cells and low affinity receptors on lymphocytes
"Structure-based modeling of the ligand binding domain of the human cell surface receptor CD23 and comparison of two independently derived molecular models.";

Protein Sci. 5:20-47(1996).

-!- FUNCTION: This receptor has essential roles in the regulation of IGE production and in the differentiation of B-cells (it is a B-cell-specific antigen).

-!- SUBCELBUAR LOCATION: TYPE II MEMBRANE PROTEIN, ALSO EXISTS AS A SOLUBLE EXCRETED FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. ..) (POTENTIAL).
MEEGGYS -> MNPPRQ (in isoform B).
//FIG4VSP 003057.
//FIG4VSP 003057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prints, Profess, lectin c; 1.

PRINTS, PR00356; ANTIFREEZEII.

PROSITE; PR0034; CLECT; 1.

PROSITE; PS00015; C_TYPE_LECTIN 1; 1.

PROSITE; PS50041; C_TYPE_LECTIN 2; 1.

Receptor; Antigen; TgE-binding protein; Repeat; Signal-anchor; Transmembrane; Lectin; Glycoprotein; Alternative splicing;
                                                                                                                                                                                                                   SMILARITY: Contains 1 C-type lectin family domain. DATABASE: NAME=PROW; NOTE=CD guide CD23 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd23.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEMBRANE BOUND FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (C-TYPE LECTIN (CLEAVAGE)
                                                                                                                                                       IsoId=P06734-2; Sequence=VSP_003057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY.
SIMILARITY.
                                                                                                                      Name=A;
IsoId=P06734-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOLUBLE FORM CYTOPLASMIC
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CHAIN
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VARSPLIC
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STRAND
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REPEAT
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Gaps
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: UME5/SRB10 and UME3/SRB11 form a kinase-cyclin pair in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuchin S., Yeghiayan P., Carlson M.;
"Cyclin-dependent protein kinase and cyclin homologs SSN3 and SSN8
contribute to transcriptional control in yeast.";
Proc. Natl. Acad. Sci. U.S.A. 92:4006-4010(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FB-2004 (Rel. 43, Last annotation update)
FNAR-2004 (Rel. 11 holoenzyme cyclin-like subunit.
UME3 OR SSN8 OR SFB11 OR YNLO25C OR N2805.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liao S.-M., Zhang J., Jeffrey D.A., Koleske A.J., Thompson C.M., Chao D.M., Viljoen M., van Vuuren H.J.J., Young R.A.; M. Kinase-cyclin pair in the RNA polymerase II holoenzyme."; Nature 374:193-196 (1995).
                                                                                                                                                 ;
0
                                                                            Length 321;
                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith J.B., Mallory M.J., Strich R., Submitted (XXX-1995) to the EMBL/GenBank/DDBJ databases.
36468 MW; F86708C0E6515B87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                 Score 25; DB 1; L
Pred. No. 3.6e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 AA
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-!- COFACTOR:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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RIR2 ASFM2
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                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MIDDLINE=80404343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Kletchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Mokenney K., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Feterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterbäck T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
the RNA polymerase II holoenzyme, and are essential for a normal transcriptional response to galactose induction in vivo, and are involved in CTD (carboxy-terminal domain) phosphorylation and this modification has a role in the response to transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                    SUBCELLULAR LOCATION: Nuclear (Potential). SIMILARITY: Belongs to the cyclin family. Cyclin C subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                           323 AA; 37790 MW; 2BA16A3374CCF207 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Transcription initiation factor IIB (TFIIB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 AA
                                                                                                                                                                                                                                                                                                                              GO, GO:0007126; P:meiosis; IGI.
InterPro; IPR006670; Cyclin.
InterPro; IPR006671; Cyclin.N.
PF00134; Cyclin, 1.
SWART; SM00385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaeoglobaceae; Archaeoglobus.
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(Rel. 40, Last seqn
(Rel. 41, Last anno
                                                                                                                                                                                                                    EMBL; U20221; AAA69820.1; -.
EMBL; U16248; AAA64270.1; -.
EMBL; U20655; AAA85744.1; -.
EMBL; Z71301; CAA5887.1; -.
PIR; S59373; S59373.
GermOnline; 143032; -.
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nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclin; Nuclear protein
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Archaeoglobus fulgidus.
                                                          regulators in vivo.
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150 PEFIPPDP 157
                                                                                                                                                                                                                                                                                                   TRANSFAC, T02155; -. SGD; S0004970; SSN8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TF2B ARCFU
028970;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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-!- SUBUNIT: Heterodimer of a large and a small chain.
-!- SIMILARITY: Belongs to the ribonucleoside diphosphate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P29095, 1AIS.

TIGR; AF1299; -
HAMAP, MF 000383; -; 1.

INTERPO: IPR0006670; Cyclin.

INTERPO: IPR000812; TFIIB euk.

Pfam; PF00382; transcript Fac2; 2.

PRINTS; PR000685; TFACTORIB.

SMART; SM00385; CYCLIN. 2.

PROSITE; PS00782; TFIIB; 2.

Transcription regulation; Repeat; Zinc-finger; Metal-binding; Zinc;
FUNCTION: Stabilizes TBP binding to an archaeal box-A promoter. Also responsible for recruiting RNA polymerase II to the preintintation complex (DNA-TBP-TFIB) (By similarity).

COFACTOR: Binds 1 zinc ion per subunit (By similarity).

SIMILARITY: Belongs to the TFIIB family.
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MEDLINE=91335775, PubMed=1871976;

BOUTSNEIL M., Shaw K., Yanez R.J., Vinuela E., Dixon L.,

Montanell M., Shaw K., Yanez R.J., Vinuela E., Dixon L.,

"The sequences of the ribonucleotide reductase genes from African
swine fever virus show considerable homology with those of the
orthopoxvirus, vaccinia virus.";

Virology 184:411-416(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- FUNCTION: Provides the precursors necessary for DNA synthesis.
-:- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside diphosphate + oxidi
thioredoxin + H(2)O = ribonucleoside diphosphate + reduced
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01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribonucleoside-diphosphate reductase small chain (BC 1.17.4.1)
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African swine fever virus (isolate Malawi Lil 20/1) (ASFV).

Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus.

NCBI_TaxID=10500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thioredoxin.
COFACTOR: Binds 2 iron ions per subunit (By similarity).
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ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
4, 9015FE14E00A31E1 CRC64;
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Pred. No. 3.7e+02;
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4; Mismatches
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226
318
30
33
49
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45 GEFICQDC 52
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ZN FING 30
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Bacteriol. 184:4601-4611(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-2004 (Rel. 43, Last annotation update)
CDP-6-deoxy-L-threo-D-glycero-4-hexulose-3-dehydrase reductase (CDP-6-deoxy-delta-3,4-glucoseen reductase) (EC 1.17.1.-) (E3).
ASCD OR RFBI OR YPO3116 OR Y1067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., Perry R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-Y peetis; STRAIN=CO-92 / Biovar Orientalis; MEDLINE=21470413; PubMed=11586360; MEDLINE=21470413; PubMed=11586360; MEDLINE=21470413; PubMed=11586360; MEDLINE=21470413; PubMed=11586360; Mischill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyhere A.V., Leather S., Moule S., Oyston P.C.F., Quall M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yersinia pseudotuberculosis,
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                             HSSP, B1157; IXSM.

InterPro; INSO 1358; Ribonucl redetse.

Pfam; PF002568; RIBORD SMALL; 1.

R PROSITE; PS00368; RIBORED SMALL; 1.

WAIDAL 101 101 IRON 1 (BY SIMILARITY).

FT METAL 104 104 IRON 2 (BY SIMILARITY).

FT METAL 109 1198 IRON 2 (BY SIMILARITY).

FT METAL 109 IRON 2 (BY SIMILARITY).

FT METAL 198 IRON 2 (BY SIMILARITY).

FT METAL 198 IRON 2 (BY SIMILARITY).

FT METAL 198 IRON 2 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 1; Length 327;
Pred. No. 3.7e+02;
Mismatches 0; Indels
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SPECIES=Y.pestis; STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 3.7e
4; Mismatches
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                                                                                                                                                                                                                          EMBL; M64728; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38966 MW;
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50.0%; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
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small chain family
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191 NEFISRDE 198
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Best Local Similarity
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                                                                                                     Lo S.F., Miller V.P., Lei Y., Thorson J.S., Liu H.-W., Schottel J.L., "CDP-6-deoxy-delta 3,4-glucoseen reductase from Yersinia pseudotuberculosis: enzyme purification and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: PARTICIPATES IN THE CONVERSION OF CDP-6-DEOXY-D-GLYCERO-L-THREO-4-HEXULOSE TO 3,6-DIDEOXY-D-GLYCERO-D-GLYCERO-4-HEXULOSE TOGETHER WITH CDP-6-DEOXY-D-GLYCERO-L-THREO-4-HEXULOSE-3-DEHYDRASE (E1) IN TWO CONSECUTIVE STEPS. THE DETAILED MECHANISM OF E3 IS NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thorson J.S., Lo S.F., Ploux O., He X., Liu H.-W.;
"Studies of the biosynthesis of 3,6-dideoxyhexoses: molecular cloning
and characterization of the asc (ascarylose) region from Yersinia
pseudotuberculosis serogroup VA.";
J. Bacteriol. 176:5483-5493(1994).
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-!- SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=Y.pseudotuberculosis;
MEDLINE=97121283; PubMed=8961949;
Vobnson D.A., Gassner G.T., Bandarian V., Ruzicka F.J., Ballou D.P.,
Reed G.H., Liu H.-W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Kinetic characterization of an organic radical in the ascarylose biosynthetic pathway."; Biochemistry 35:15846-15856(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=Y.pseudocuberculosis;
MEDLINE=96664885; PubMed=8672475;
Gassner GT., Johnson D.A., Liu H.-W., Ballou D.P.;
"Kinetics of the reductive half-reaction of the iron-sulfur flavoenzyme CDP-6-deoxy-L-threo-D-glycero-4-hexulose-3-dehydrase
                                                                                                                                                                                                                                                                                                                                                                                                                                 Kessler A.C., Haase A., Reeves P.R.; "Molecular analysis of the 3,6-dideoxyhexose pathway genes of
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=M85 / Serotype IIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECTENCE FROM N.A.
SPECIES-Y.pseudotuberculosis; STRAIN-Serotype VA;
MEDLINE=94350832; PubMed-8071227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yersinia pseudotuberculosis serogroup IIA.";
J. Bacteriol. 175:1412-1422(1993).
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. SPECIES=Y.pseudotuberculosis; STRAIN=V; MEDLINE=94117382; PubMed=8288541;
                                                                                                                                                                                                                                                                                                                                                         SPECIES=Y.pseudotuberculosis; STR
MEDLINE=93186709; PubMed=8444803;
                                                                                                                                                                                                                                                        Bacteriol, 176:460-468(1994).
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PIR; AE0378; AE0378.
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                                                                                                                                                                                                                          cloned gene.";
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Aldredge T., Bashizadeh R., Blakely D., Cook R., Gilbert K.,

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Spadafora R., Wang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155 (1997).

I. FUNCTION: Catalyzes the oxidation of 3-carboxy-2-hydroxy-4-methylpentanoate (3-isopropylmalate) to 3-carboxy-4-methyl-2-
                                                                                                                          pfam; PF00111; fer2; 1.
Pfam; PF00175; NAD binding_1; 1.
PRINTS; PR00371; FFBKTR.
PRINTS; PR00410; PFBKTR.
PROSTE; PS00197; 2PE2S FERREDOXIN; 1.
Oxidoreductase; Electron transport; Metal-binding; Iron-sulfur; Iron;
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-!- PATHWAY: Leucine biosynthesis; third step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the isocitrate and isopropylmalate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxopentanoate. The product decarboxylates to 4-methyl-Z
                                                                                                                                                                                                                                                                                                                                                                ; Score 25; DB 1; Length 328; Pred. No. 3.7e+02; 4; Mismatches 0; Indels
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
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                                                          InterPro; IPR001709; FPN cyt redctse.
InterPro; IPR001433; Oxred FAD/NAD(P)
InterPro; IPR001221; Phe hydroxylase.
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FAD binding 6.
Ferredoxin.
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INIT MET 0 0
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             InterPro; IPR006058;
                              InterPro; IPR008333;
                                             InterPro; IPR001041;
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Best Local Similarity
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or send an email to license@isb-sib.ch).
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Pfam; PF00180; isodh; 1.
PR0SITE; PS00470; IDH IMDH; 1.
Oxidoreductase; Leucine biosynthesis; NAD; Complete proteome.
SEQUENCE 329 AA; 35785 MW; E56803788013E5CF CRC64;
                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 25; DB 1; Length 329;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 4; Mismatches 0; Indels
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PIR; F69051; F69051.
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**BLOSUM62DX** Scoring table: 1017041 seqs, 315518202 residues Searched:

Gapop 10.0 , Gapext 0.5

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 300 summaries

sp archea:\*
sp bacteria:\*
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sp invertebrate:\*
sp mammal:\*
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sp organelle:\*
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sp\_virus:\* SPTREMBL 110:: 112:: 123:: 124:: 125:: 126:: 1 Database :

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SUMMARIES		ID	005663	090XA9	090XC5	08EX80	OPRIKO	09AZH6	O8L2B1	ORXII.19	CWAT-90	09824R	019347	097N33	CONTRO	095570	ORRHAR	031516
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Q8v3k6 swinepox vi Q91ms0 lumpy skin Q8jts8 lumpy skin Q8dqi3 chlamydomon Q97ec0 clostridium Q9fwi7 oryza sativ Q7kmi3 oryza sativ Q8wy2 lactobacill Q81w38 bacillus an Q81zv8 bacillus an Q81zv8 bacillus an Q81zv8 pacillus an Q81zv8 pacillus an Q81zv8 pacillus an	Q89940 burkholderi Q89ja6 xanthomonas Q8et09 oceanobacil Q9gjy0 oryctolagus Q71ff gallus gall Q93eh4 helicobacte Q24060 drosophila Q849f7 venorhabdi Q849f7 vibrio vuln Q24077 drosophila Q24077 acinetobact Q24077 acinetobact	092528 carnation 1 08311 carnation 1 08311 carnation 1 08315 pseudomonas 082973 bacillus sp 086394 cira barbar 086394 cira barbar 086394 lutra lutra 086392 lutra macul 086393 lutra macul 086399 aonyx capen 086399 anblonyx ci 086397 chiydra lut 086397 chiydra lut 086397 lontra feli 086397 lontra long 086399 lontra long	stel stel stel rtes rtes loga ssar scyo crep	Q83up9 gamma-prote Q8hBh2 oryza sativ Q8hBh2 oryza sativ Q9m9m6 arabidopsis Q8g2v8 brucella su Q9azu2 bacteriopha Q9cfq8 lactococcus Q9ltr0 arabidopsis Q8xc01 escherichia Q7vbn6 prochloroco Q8lvi3 bacillus an Q8livi3 bacillus ce Q9km48 vibrio chol Q8gm0 streptomyce Q8ex15 mycoplasma Q97e59 clostridium
Q8V3K6 Q91MSO Q8UTS8 Q84Q13 Q97KH23 Q9FW17 Q9FW17 Q81W22 Q81W38 Q95HS2 Q81UA6 Q95HS2 Q8UIA6	QSE1940 QSE706 QSE370 QSG370 QSG3714 QS3714 QS13614 QSB377 QSB377 QSB377 QC4077 QC4077 QC4077	092528 092528 088741 088741 086390 086390 086302 086302 086302 086302 086304 086304	Q863P8 Q863P8 Q863P8 Q863P8 Q863P9 Q863P2 Q863P0 Q863P0 Q863N6 Q80TTO Q8XVS QVIXS	Q83UP9 Q84BH2 Q44BH2 Q94BH2 Q9M9M6 Q9M2ZZQ Q9CZQB Q9LTRO Q9LTRO Q1VTBO Q81VT3 Q9RMDB Q81W3 Q9RMDB Q8GGNO QBEX15
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O7vt94 bordetella
O8w5v5 bacteriopha
O9m5v5 bacteriopha
O9pd90 xylella fas
O9bty7 rhizobium 1
O8cv08 oceanobacil
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O9cy45 mus musculu
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Q7wsf6 bordetella
Q7vz56 bordetella
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                    092gw7 rickettsia
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087a23 xylella fas
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09pa77 xylella fas
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MEDLINE=96285745; PubMed=8725005;

MEDLINE=96285745; PubMed=8725005;

Becker J., Brandel M.;

"Molecular cloning and characterization of the pyrB gene of
Eactobecillus letchmannii encoding aspartate transcarbamylase.";

Biochimie 78:3-3(1996).

EMBL, X84262; CAA59022.1; -.

InterPro; IPR005847; Pept_M38_regn.

Probom; P0000518; Urease; 1.

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Stein S., Liehr T., Eschrich K.;
"Characterization of the mouse liver fructose-1,6-bisphosphatase
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900; GO:00442132; F:functose-bisphosphatase activity; IEA.

GO: GO:0016787; F:hydrolase activity; IEA.

GO: GO:0042578; F:hydrolase activity; IEA.

GO: GO:004578; F:phosphoric ester hydrolase activity; IEA.

GO: GO:005975; P:arbohydrate metabolism; IEA.

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4; Mismatches 0; Indels
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Lactobacillus leichmannii.
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Lactobacillus
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Last annotation update)
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HSSP; P00636; 1CNQ.
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4; Conservative 4;
01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-OCT-2003 (TrEMBLrel. 25,
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01-OCT-2003 (TrEMBLrel. 25,
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TISSUE=Liver;
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39 AA;
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MEDLINE=21113149; PubMed=11160885;
Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.;
Analysis of six prophages in Lactococcus lactis IL1403: different
genetic structure of temperate and virulent phage populations.";
Nucleic Acids Res. 29:644-651(2001).
  ORF5.
Bacteriophage bIL311.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
   SEQUENCE FROM N.A. COTOKIN A., Ehrlich S.D., Chopin M.-C.; Chopin A., Bolotin A., Sorokin EMBL/GenBank/DDBJ databases. Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF323672; AAK08437.1; --
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GO, GO:0005524; FATP binding; IEA.
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GO, GO:0006260; P:DNA replication; IEA.
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Last annotation update)
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(TrEMBLrel. 17, I
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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GO; GO:00421379; F:fydrolase activity; IEA.

GO; GO:0042578; F:phosphoric ester hydrolase activity; IEA.

GO; GO:0005975; F:carbohydrate metabolism; IEA.

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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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  Gene 264:215-224(2001)
   Hypothetical protein.
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  1 GEFIMVDR 8
  Local Similarity
es 4; Conser
   SEQUENCE FROM N.A.
  1 XEFIXXDX
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50.0%;
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   SEQUENCE
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  Nozue H., Tsuchiya K., Kamio Y., "Nucleotide sequence and copy control function of the extension of the incl region (incl-b) of Rtsl."; Plasmid 19:46-56(1988).
   MEDLINE=94358883; PubMed=8078071;
Janosi L., Yonemitsu H., Hong H., Kaji A.;
"Molecular cloning and expression of a novel hydroxymethylcytosine-
specific restriction enzyme (PvuRtsII) modulated by glucosylation of
   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Murata T., Ohnishi M., Ara T., Kaneko J., Han C.-G., Li Y.F., Takashima K., Nojima H., Nakayama K., Kaji A., Kamio Y., Miki T., Morti H., Ohtsubo E., Terawaki Y., Hayashi T.; "Complete Nucleotide Sequence of Plasmid Rts1: Implications for Bvolution of Large Plasmid Genomes.";

J. Bacteriol. 184:3194-3202(2002).
   Mochida S., Tsuchiya H., Mori K., Kaji A.;
"Three short fragments of Rts1 DNA are responsible for the
temperature-sensitive growth phenotype (tsg) of host bacteria.";
J. Bacteriol. 173:2600-2607(1991).
   Tian Q.B., Ohnishi M., Tabuchi A., Terawaki Y.,
"A new plasmid-encoded proteic killer gene system: cloning, sequencing, and analyzing hig locus of plasmid Rtsl.",
Biochem. Biophys. Res. Commun. 220:280-284(1996).
  Murata T., Hayashi T.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
  STRAIN=UR-75;
MEDLINE=88139175; PubMed=3277947;
Tanaka M., Okawa N., Mori K., Suyama Y., Kaji A.;
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MEDLINE=22024716; PubMed=12029035;
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  MEDLINE=91193219; PubMed=2013575;
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MEDLINE=88289863; PubMed=2840681;
  Mol. Biol. 242:45-61(1994).
  22,
22,
24,
  Enterobacteriaceae, Proteus.
  PRELIMINARY;
   01-OCT-2002 (TrEMBLrel. 01-JUN-2003 (TrEMBLrel.
   01-OCT-2002 (TrEMBLrel.
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2 TEFITIDE 9
   Arsenate reductase.
ORF90.
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   STRAIN=UR-75;
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Terawaki Y., Kakizawa Y., Takayasu H., Yoshikawa M.;
"Temperature sensitivity of cell growth in Escherichia coli associated with the temperature sensitive R(KM) factor.";
Wature 219:284-285(1968)
Mature 219:284-285(1968)
EMBL; AP004237; BAB93653.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
'Nucleotide sequence of an Rts1 fragment causing temperature-dependent
   Gaps
   Kamio Y., Terawaki Y.;
"Nucleotide sequence of an incompatibility region of mini-Rts1 that
contains five direct repeats.";
J. Bacteriol. 155:1185-1191(1983).
   MEDLINE=84185439; PubMed=6325393; Mamio Y., Tabuchi, A., Itch Y., Katagiri H., Terawaki Y.; "Complete nucleotide sequence of mini-Rts1 and its copy mutant."; Bacteriol. 158:307-312(1984)
   Mollet B., Clerget M., Meyer J., Tida S., "Organization of the The-related kanamycin resistance transposon Tn2660 carrying two copies of IS26 and an IS903 variant, IS903. J. Bacteriol 163:55-60(1985).
  Salanoubat M., Genin S., Attiguenave F., Gouzy J., Mangenot S., Alata M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Fenard C., Cunnarc S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Weissenbach J., Boucher C.A., Mincker P., Levy M., "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
  .;
   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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  Score 25; DB 2; Lenguary No. 5.4e+02; O; Indels
  Length 57;
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  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
  Ralstonia solanacearum (Pseudomonas solanacearum)
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4; Mismatches
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J. Bacteriol. 170:1175-1182(1988).
   MEDLINE=85234397; PubMed=2989253;
  STRAIN=GMI1000,
MEDLINE=21681879; PubMed=11823852;
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  01-MAR-2002 (TrEMBLrel. 20, L
Hypothetical protein RSc3189.
RSC3189 OR RS06087.
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Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
   Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium.
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   Fraser D.G., Bailey E.;
"Polymorphism and multiple loci for the horse DQA gene.";
Immunogenetics 47:487-490(1998).
EMBL; U92514; AAC17578.1; -.
EMBL; U92514; AAC17578.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:006995; P:immune response; IEA.
InterPro; IPRO01003; MHC II alpha.
Pfam; PF00993; MHC II alpha; 1.
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S 68
SEQÜENCE 68 AA; 7992 MW; 8A522AF80CC51581 CRC64;
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50.0%; Pred. No. 6.5e+02;
tive 4; Mismatches 0; Indels
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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GO; GO:0006955; P:immune response; IEA.
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Pfam; PF00993; MHC_II_alpha; 1.
NON_TER 1 68 68
  Created)
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40 SEFISFDP 47
  : | | | :: |:
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AC 097N3
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SETQIONCE FROM N.A.
STRAIN=22491, 'Serrotroup A / Serrotype 4A;
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Parkhill J., Achruan M., James K.D., Bentley S.D., Churcher C.,
Raes S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quall M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.; train of Neisseria
meningitidis 22491.";
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
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0
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
Neisseriaceae, Neisseria.
NCBI_TaxID=65699;
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Frager D.G., Bailey E.;
"Extensive Polymorphism at the Horse DQA Locus.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF115325; AAD19975.1;
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EMBL; AL162754; CAB84063.1; -.

PIN; E81922; E81922.

Hypothetical protein; Complete proteome.

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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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   098248;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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   Conservative
  PRELIMINARY;
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16 YEFIFPDQ 23
  :|||::|:
EEFIRSDV 42
   1 XEFIXXDX 8
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Best Local Similarity
Matches 4; Conserv
  SEQUENCE FROM N.A.
  Query Match
Best Local Similarity
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STRAIN-ATCC 25586;

MEDLINE=21886394; PubMed=11889109;

MEDLINE=21886394; PubMed=11889109;

MEDLINE=21886394; PubMed=11889109;

MEDLINE=21886394; PubMed=11, Ivanova N., Reznik G., Los T., Lykidis A., Battacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Tyrpides N., Overbeek R.;

"Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586.";

J. Bacteriol. 184:2005-2018 (2002).

GO: GO: 0003723; F:RAA binding; IEA.

InterPro; IPR002942; S4.
  Sampei G., Motomura K., Masuda S., Yamaguchi T., Ando K., Oishi T., Furuya N., Komano T., Mizobuchi K.; "Organization and diversification of plasmid genomes: complete nucleotide sequence of the R721 genome."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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50.0%; Pred. No. 6.8e+02;
ive 4; Mismatches 0; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical cytosolic protein FN2129.
  Kim S., Komano T.;
"Nucleotide sequence of the R721 shufflon.";
"Bacteriol. 174:7053-7058 (1992).
EMBL, AP002527; BAB12596.1; -.
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SEQUENCE 71 AA, 8334 MW, B2551547303
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MEDLINE=93015772; Pubmed=1400257;
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STRAIN=K-12; TRANSPOSON=Tn7;
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PROSITE; PS50889; S4; 1.
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57 DEFIENDF 64
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11 TEFIKLDQ 18
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   NCBI_TaxID=562;
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  SEQUENCE
   SEQUENCE
   Plasmid,
  Query Match
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  RESULT 15
  Matches
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Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin B.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMB., AE007513, ARX7990.1;
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G0; G0:0003723; F:RNA binding; IEA.
PROSITE: PSO8889; S4; 1.
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MEDLINE-21664373; PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
  Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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   ·.
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PROSITE; PS50889; S4: 1.
Hypothetical protein; Complete proteome.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
  flesh-eater ";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP003185; BAB79709.1; -.
GO; GO:003723; F:RNA binding; IEA.
InterPro; IPR002942; S4.
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   Created)
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8 TEFIKLDS 15
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STRAIN=13 / Type A;
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SEQUENCE 68 AA;
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Best Local Similarity
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   Best Local Similarity
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  YaiA protein.
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   Q9F572;
  Q8XPG0;
  OBXPG0
   Q9F572
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RESULT 14
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25 YEFITDDE 32
  1 XEFIXXDX 8
   1 XEFIXXDX 8
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ID Q8JTS
AC Q8JTS
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  RESULT 18
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  Gaps
  Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
   MEDLINE-21624277; Pubmed-11752168;
Afonso C.L., Tulman E.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
Kutish G.F., Rock D.L.;
   Afonso C.L., Tulman B.R., Lu Z., Balinsky C., Osorio F.A., Zsak L.,
Kutish G.F., Rock D.L.;
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neotteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha; Cyprinodontiformes, Poeciliidae, Poecilia.
  MEDLINE=9612821; PubMed=8537120;

MEDLINE=9612821; PubMed=8537120;
Sato A., Figueroa F., O'Hugin C., Reznick, Klein J.,

Identification of major histocompatibility complex genes in the guppy, Poecilia reticulata.",

Immunogenetics 43:38-49(1996).

EMBL; Z84079; CA840785.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016221; C:integral to membrane; IEA.

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GO; GO:0019886; P:antigen presentation, exogenous antigen via M.

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Kara P.D., Afonso. C.L., Wallace D.B., Kutish G.F., Stipinovich C.,
Lu Z., Vreede F.T., Taljaard L.C.F., Zsak A., Viljoen G.J., Rock D.L.;
"Molecular characterization of the South African vaccine strain and
the field isolate of lumpy skin disease virus.";
Submitted (AUG-2001) to the BBEL/GenBank/DDBJ databases.
EMBL; AF325528; AAK85054.1;
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MEDLINE=21329459; PubMed=11435593;
Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"Genome of lumpy skin disease virus.";
J. Virol. 75:7122-7130(2001).
  SEQUENCE FROM N.A. STRAIN=Neethling 2490; Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR007952; Pox A3L.
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01-DEC-2001 (TrEMBLrel. 19, Created)
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Matches

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Noblling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing bacterium Clostiidium acetobutylicum.";
   SEQUENCE FROM N.A. Wing R.A. Frisch D., Presting G., Wood T., Yu Y., Rambo T., Crane Schwartzbeck J., Thurmond S., Mao D.;
  Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
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EMBL; AC031197; AAG12482.2;
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SEQUENCE 80 AA; 8891 MW; 98F6D664F8B95709 CRC64;
   J. Bacteriol. 188:4823-4838(2001).

EMBL, AE007814; AAK81130.1; -.

PIR, G97292; G97292.

Hypothetical protein; Complete proteome.

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Last annotation update)
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  PRT;
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  STRAIN-Neethling vaccine LW 1959;

Kara P.D., Afonso C.L., Wallace D.B., Kutish G.F., Stipinovich C.,
Lu Z., Vreede F.T., Taljaard L.C.F., Zsak A., Viljoen G.J., Rock D.L.,
"Molecular characterization of the South African vaccine strain and
   Gaps
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            Lumpy skin disease virus (LSDV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
   Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta; Chlorophyceae; Volvocales;
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   the field isolate of lumpy skin disease virus.";
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EMBL; AF409138; AAN02818.1;
  75 AA; 9022 MW; 98A41C4CAF4FECF6 CRC64;
  Cenkci B., Petersen J.L., Small G.D.,
"REX1, a novel gene required for DNA repair.";
Biol. Chem. 0:0-0(2003).
EMBL, AY236491, AP212520.1;
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Last annotation update)
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Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

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Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,

Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,

Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,

Fraser C.M.;
  MEDIJINE—2.2. Sorokin A., Anderson I., Galleron N., Candelon B., Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mithailova N., Lapidus A., Chu L., Mazur M., Goltsman B., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N., "Genome sequence of Bacillus cereus and comparative analysis with
  "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
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(TrEMBLrel. 24, Last annotation update)
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  Nature 423:87-91(2003)
EMBL; AE017010; AAP10855.1; -.
   Nature 423:81-86(2003).
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6 MEFIKADE 13
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Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Klipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
Fleirs M.W. B.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vies M., Ursing
De Vos W.M., Siezen R.J.;
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   "Complete genome sequence of Lactobacillus plantarum WCFS1.";
Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
EMBI, AL932525; CAD63935.1; -.
GQ; GO:0006790; P:sulfur metabolism; IEA.
InterPro; IPR003749; This.
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Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, ABC17048; AAP51792.1; -.
Hypothetical protein.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
Molybdopterin biosynthesis protein, D chain.
   81 AA.
  4; Mismatches
   Pred. No.
   Created)
   PRT;
  Hypothetical protein.
BA4145.
Bacillus anthracis (strain Ames).
   100.0%;
50.0%; E
  100.08;
   50.0%;
   Science 300:1566-1569(2003).
  4; Conservative
   PRELIMINARY;
   01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
   4; Conservative
  PRELIMINARY;
   Pfam, PF02597; This; 1.
Complete proteome.
                 STRAIN=cv. Nipponbare;
  : | | | :: | :
56 QEFIADDR 63
   : | | | :: |:
32 VEFIAADM 39
  1 XEFIXXDX 8
   1 XEFIXXDX 8
  Query Match
Best Local Similarity
   Query Match
Best Local Similarity
  FROM N.A.
   SEQUENCE FROM N.A.
   NCBI_TaxID=1590;
   MOAD OR LP 1479
  chromosome 10
  SEQUENCE
  SEQUENCE
  Q81W38;
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Q88WY2;

Q88WY2

RESULT 24

Q88WY2

Matches

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Gaps

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Gaps

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Q81W38

RESULT 25

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Q81W38

Matches

01-DEC-2001 01-DEC-2001

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SPECIES=B.cepacia; STRAIN=JS150; Kahng H.Y., Kukor J.J.; "Genetic and functional analysis of Tbc monooxygenases for catabolism of alkyl- and chloroaromatic compounds in Burkholderia cepacia JS150.";
   Ayoubi P.J., Harker A.R.,
"Whole-cell kinetics of trichloroethylene degradation by phenol
hydroxylase in a raistonia eutropha JMP134 derivative.";
Appl. Environ. Microbiol. 64:4353-4356 (1998).
EMBL; AF065891; AAC77381.1;
   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
  Burkholderia pickettii (Pseudomonas pickettii), and
Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
   100.0%; Score 25; DB 2; Length 86; 50.0%; Pred. No. 8.3e+02; tive 4; Mismatches 0; Indels
   SEQUENCE FROM N.A.
SPECIES=B.pickettii; STRAIN=PKO1;
SPECIES=B.pickettii; STRAIN=PKO1;
SPECIES=B.pickettii; STRAIN=PKO1;
Byrne A.M., Kukor J.J., Olsen R.H.;
"Sequence analysis of the gene cluster encoding toluene-3-monooxygenase from Pseudomonas pickettii PKO1.";
Gene 154:65-70(1995).
   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
   891; AAC77381.1; -.
86 AA; 9583 MW; 6F9E4D89D5C00840 CRC64;
   EMBL, U04052; AAB99619-1, -.
EMBL; AF28289; AAG40795.1; -.
GO:0004497; F:monooxygenase activity; IEA.
Hypothetical protein; Monooxygenase.
SEQUENCE 86 AA; 9604 MW; 7D50901A65635AB3 CRC64;
  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
  Last sequence update)
Last annotation update)
   100.0%; Score 25; DB 2;
50.0%; Pred. No. 8.3e+02;
tive 4; Mismatches 0;
  86 AA.
   Alcaligenes eutrophus (Ralstonia eutropha)
   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence v
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Hypothetical protein (Tbc2B monoxygenase).
   Putative hydroxylase component.
  100.08;
   Query Match
Best Local Similarity 50.00,
4; Conservative
  PRELIMINARY;
   Query Match
Best Local Similarity 50.0°
Matches 4; Conservative
  PRELIMINARY:
   79 LEFIFCDA 86
   NCBI_TaxID=329, 292;
   1 XEFIXXDX 8
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   NCBI_TaxID=510;
   PubMed=9797289;
  STRAIN=JMP134;
   TBUU OR TBC2B.
   RESUL
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   051940
  RESULT 30
   051940
  ACCOORDING SERVICE SER
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  . .; IEA.
  Richman A.D., Herrera L.G., Nash D.;

"MHC Class II Beta Sequence Diversity in the Deermouse (Percomyscus maniculatus): Implications for Models of Balancing Selection.";

"MHC Class II Beta Sequence Diversity in the Deermouse (Percomyscus maniculatus): Implications for Models of Balancing Selection.";

"Balancited (OCT_2000) to the EMBL/GenBank/DDBJ databases.

"BABL; AF312753; AAK98053.1;

"BABL; AF312753; AAK98053.1;

"BAG); GO:0016021; C:integral to membrane; IEA.

"BAG); GO:0015081; F:MHC class II receptor activity; IEA.

"BAG); GO:0019884; P:antigen presentation, exogenous antigen; IEA.

"BAG); GO:0006959; P:immune response; IEA.

"BAG); GO:0006959; P:immune response; IEA.

"BAG); BAG); P:Immune response; IEA.
  Gaps
   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
   Gaps
   Peromyscus maniculatus (Deer mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Sigmodontinae;
  0;
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   STRAIN-VCI / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE010237; AAL81439.1;
InterPro: IRR004919; DUFF62.
IRR0FAPO: IDPF62: 1
HYPOthetical protein; Complete proteome.
SEQUENCE 85 AA; 9960 MW; B3CE50A6CFF33C4F CRC64;
  100.0%; Score 25; DB 17; Length 85; 50.0%; Pred. No. 8.2e+02; ive 4; Mismatches 0; Indels
  Score 25, DB 7; Length 85;
Pred. No. 8.2e+02;
4; Mismatches 0; Indels
   Indels
  85 AA; 10237 MW; 3061A008A7BE71DB CRC64;
-DEC-2001 (TrEMBLrel. 19, Created)
-DEC-2001 (TrEMBLrel. 19, Last sequence update)
-JUN-2003 (TrEMBLrel. 24, Last annotation update)
   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PF1315.
  01-JUN-2003 (TrEMBLrel. 24, Labe ammiliant).
MHC class II antigen beta chain (Fragment).
  85 AA.
   4; Mismatches
   100.0%;
  50.0%;
   Query Match
Best Local Similarity 50.00.
  4; Conservative
  PRELIMINARY;
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26 EEFIRFDS 33
  :|||::|:
EEFITDDP 63
   1 XEFIXXDX 8
  Pyrococcus furiosus
   1 XEFIXXDX 8
   SEQUENCE FROM N.A.
   NCBI_TaxID=10042;
   Best Local Similarity
   SEQUENCE FROM N.A.
   NCBI_TaxID=2261;
   STRAIN=SQPM26a;
   85
  Peromyscus.
   Pyrococcus
  NON TER
SEQUENCE
   26
  Query Match
  NON TER
   Q8U1A6
Q8U1A6;
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RESULT 28

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Length 86; 0; Indels

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Ouyang J., Nie Q., Zhang X.;
   : | | | :: | :
39 GEFILVDK 46
  HEFIARDV 15
   1 XEFIXXDX 8
   1 XEFIXXDX 8
  SEQUENCE FROM N.A.
   Gallus.
NCBI_TaxID=9031;
   NCBI_TaxID=9986;
   91
   NON TER
NON TER
SEQUENCE
  Hydrolase
  Q7T1F7
   RESULT 34
   RESULT 33
   Q7T1F7
   OBGUYO
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   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 202145; PubMed=12024217;

MEDINE=2202145; PubMed=12024217;

A a Silva A.C.R., Ferro J.A., Rethach F.C., Farah C.S., Furlan L.R.,

A ca silva A.C.R., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A lves L.M.C., do Amaral A.M., Bertolini M.C., Camargo, L.E.A.,

A lves L.M.C., do Amaral A.M., Derlini M.C., Camargo, L.E.A.,

A camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A camarotte G., Cannavan F., Cardozo J., Chambergo F., El-Dorry H.,

A carai J.B., Ferraco M.C., Greggio C.C., Ferro M.I.T.,

A principle F., Franco M.C., Greggio C.C., Gruber A.,

Rotsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

A carai J.B., Mardanis J., Menck C.F.M., Mayaki C.Y., Moon D.H.,

A martins E.C., Machadow J., Manck C., Chiveira V.R.,

A martins E.C., Machadow J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

A preira H.A., Rossi A., Sena J.A.D., Silva C., Ge Souza R.F.,

A Spinola L.A.F., Takita M.A., Tandura R.E., Teixeira E.C., Tezza R.I.D.,

A rrindade dos Santos M., Trufffi D., Tsai S.M., White F.F.,

A schubal J.C., Kitajima J.P.;

A cromparison of the genomes of two Xanthomonas pathogens with differing construction of the genomes of two Xanthomonas pathogens with differing construction of the genomes of two Xanthomonas pathogens with differing construction of the genomes of two Xanthomonas pathogens with differing construction of the genomes of two Xanthomonas pathogens with differing construction of the genomes of two Xanthomonas pathogens with differing construction of the genomes of two Xanthomonas pathogens with differing construction of the genomes of two Xanthomonas pathogens with differing construction of the genomes of two Xanthomonas pathogens with differing construction of the genomes of two Xanthomonas pathogens with differing construction of the genomes of two Xanthomonas pathogens with differing construction of the genomes of two Xanthomonas pathogens with differing construction of the genomes of two Xanthomonas pathogens 
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  SEQUENCE FROM N.A.
STRAIN=HTBB31 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus ineyensis isolated from the Iheya
   Gaps
   Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
   ;
   Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
NCBL_TaxID=182710;
   100.0%; Score 25; DB 16; Length 90; 50.0%; Pred. No. 8.7e+02;
  Ridge and its unexpected adaptive capabilities to extreme
   Indels
   Nature 417:459-463(2002).
EMBL, AE011903; AAM378.1; -.
Hypothetical protein; Camplete proteome.
SEQUENCE 90 AA; 10209 MW; D4F880AED6935695 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein XAC2631.
   , Last sequence update)
, Last annotation update)
   ..
  90 A.A.
  90 AA.
   Pred. No. 8.7e
4; Mismatches
   01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last seqn 01-WAR-2003 (TrEMBLrel. 23, Last anni Hypothetical conserved protein.
  PRT;
  50.08;
   4; Conservative
  PRELIMINARY;
  PRELIMINARY;
  :|||::|:
29 QEFIELDD 36
  1 XEFIXXDX 8
   : [||::|:
LEFIFCDA 86
                       1 XEFIXXDX 8
   Best Local Similarity
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  79
  Query Match
  Q8ET09;
  Q8ET09
  Q8PJA6;
   08PJA6
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Q8ET09
   Matches
   Q8PJA6
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   Growth hormone receptor (Fragment).
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves; Neognathae, Galliformes, Phasianidae,
   Gaps
   Gaps
  SEQUENCE FROM N.A.

"Inflaman H., Bschrich K.;

"Inflaman H., Bschrich K.;

"Inflaman H., Bschrich K.;

"Liver and muscle fructose-1,6-bisphosphatase isoenzyme amounts in different rabbit tissues.";

different rabbit tissues.";

different dibc.-2000) to the BMBL/GenBank/DDBJ databases.

EMBL, AJ300657; CAC19334.1;

HSSP; P00637; IBK4.
   Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
  ..
  .;
0
  GO; GO:0042132; F:fructose-bisphosphatase activity; IEA. GO; GO:004578; F:hydrolase activity; IEA. GO; GO:0042579; F:hydrolase activity; IEA. GO; GO:0042579; F:phosphoric ester hydrolase activity; IEA. GO; GO:0005975; P:carbohydrate metabolism; IEA. III. Therpro; IPRO0146; II. FB_phphtase.
   ; Score 25; DB 16; Length 90;
Pred. No. 8.7e+02;
4; Mismatches 0; Indels
   ; Score 25; DB 6; Length 91;
Pred. No. 8.8e+02;
4; Mismatches 0; Indels
                         EMBL, AP004594; BAC12412.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 90 AA; 10509 MW; D2647123061E723B CRC64;
  01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment)
  91 AA; 9919 MW; 3D9C4C087C09AA33 CRC64;
  01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
   92 AA.
   91 AA.
Nucleic Acids Res. 30:3927-3935(2002).
  Pfam; PF00316; FBPase; 1.
ProDom; PD001491; In FB_phphtase; 1.
   01-MAR-2001 (TrEMBLrel. 16, Created)
   100.08;
   100.0%;
50.0%;
   50.08;
   Query Match
Best Local Similarity 50.v.
Loc 4; Conservative
   Ouery Match
Best Local Similarity 50...
4; Conservative
  PRELIMINARY;
  PRELIMINARY;
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Vibrio vulnificus.
   SEQUENCE FROM N.A.
   NCBI_TaxID=672;
  Query Match
  Thomas K
   Query Match
   Q8D9P7;
   Q814L7
  08D9P7
  RESULT 37
  RESULT 38
Q8D9P7
   Q814L7
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  Gaps
   Gaps
  Helicobacter hepaticus,
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
  Ge Z., Feng Y., Fox J.G.;
"Helicobacter hepaticus genome: construction of an ordered cosmid
"Helicobacter hepaticus genome: construction of an ordered cosmid
"Helicobacter hepaticus genome: construction of an ordered cosmid
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF358631, AAL16680.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0003106; P:protein secretion; IEA.
InterPro; IFR001712; Bact_FHIPEP.
Pfam; PF00771; FHIPEP.
NOW_TER
   0;
   0
  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ecdysone-inducible protein 71EJ.
EIGTIEJ OR L71-10 OR CG7588.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota; Neoptera; Endopterygota; Diptera, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
   100.0%; Score 25; DB 13; Length 92; 50.0%; Pred. No. 8.9e+02; tive 4; Mismatches 0; Indels
  100.0%; Score 25; DB 2; Length 95; 50.0%; Pred. No. 9.2e+02; tive 4; Mismatches 0; Indels
"Sequence of cGHR intron 9.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY327492; AAP92122.1; -.
  1 1
92 92
92 AA; 10377 MW; 5F624696942A3269 CRC64;
  95 95
95 AA; 10789 MW; BED4A41B153EBA53 CRC64;
  Q93EH4;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
  95 AA
   95 AA.
   Flagellar biosynthesis protein (Fragment).
   01-NOV-1996 (TrEMBLrel. 01, Created)
  PRT;
  PRT;
  SEQUENCE FROM N.A.
STRAIN=CANTON-S;
MEDLINE=96152797; PubMed=8568884;
   Query Match
Best Local Similarity 50.00,
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   PRELIMINARY;
  : | | | : : | :
48 VEFIELDI 55
  1 XEFIXXDX 8
   10 EEFITKDE 17
  1 XEFIXXDX 8
   SEQUENCE FROM N.A.
   NCBI_TaxID=32025;
  NCBI_TaxID=7227;
  STRAIN=3B1;
   NON TER
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  NON_TER
SEQUENCE
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   024060;
   024060
   RESULT 35
093EH
AC 093EH
DT 01-DEN
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224060
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   Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
   Gaps
Wright L.G., Chen T., Thummel C.S., Guild G.M.;
"Molecular characterization of the 71E late puff in Drosophila melanogaster reveals a family of novel genes.";
J. Mol. Biol. 255:387-400 (1996).
EMBL; U23836; AAA74183.1;
EMBL; U23836; AAA74183.1;
ENBE; U23836; AAA74183.1;
InterPro; IPR001475; Insect_Unk.
Pfam; PF02448; L71;
SEQUENCE 95 AA; 11446 MW; 33171F38EA2826D1 CRC64;
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   100.0%; Score 25; DB 5; Length 95; 50.0%; Pred. No. 9.2e+02; tive 4; Mismatches 0; Indels
   Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
  Genome sequence of the nematode C.elegans: A platform for
   Length 95;
   0; Indels
   Thomas K.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
  46723F3FEBBF6189 CRC64;
  Q814L7; C1-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-WAR-2003 (TrEMBLrel. 24, Last annotation update) Hypothetical protein E02Al0.4.
  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
  // Score 25; DB 5;
Pred. No. 9.2e+02;
4; Mismatches 0;
   95 AA.
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  Plasmid stabilization system protein.
   PRT;
  PRT;
  SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
  investigating biology.";
Science 282:2012-2018(1998).
EMBL, Z81053; CAD54130.1; -.
WormPep; E02A10.4; CE31898.
Hypothetical protein.
SEQUENCE 95 AA; 10397 MW; 4.
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Matches 4; Conservative
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  PRELIMINARY;
  Caenorhabditis elegans.
  :|||::|:
46 LEFINSDC 53
  : | | | :: | :
27 EEFIAVDC 34
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   1 XEFIXXDX 8
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   STRAIN=CMCP6;
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50.0%;
   Acinetobacter calcoaceticus.
  Science 287:2185-2195(2000).
  EMBL; U24574; AAA65118.1; -. PIR; S62338; S62338.
   4; Conservative
   PRELIMINARY;
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46 LEFINSDC 53
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  Query Match
Best Local Similarity
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   SEQUENCE FROM N.A.
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   Matches
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  Gaps
  STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
   STRAIN=CMCP6;
Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choy H.E.;
  ..
Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choy H.E.;
   ..
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  EIG71EJ protein.

EIG71EJ OR L71-10 OR CG7588.

Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
NCBI_TaxID=672;
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                             "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016805; AA010901.1; -.
InterPro; IPR007712; Plasmid stabil.
Pfam; PF05016; Plasmid_stabil.
Complete proteome.
SEQUENCE 95 AA; 10992 MW; 52D1683C38E56292 CRC64;
   "Complete genome sequence of Vibrio vulnificus CMCP6."; submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE016805; AA010879.1; -.
  97 AA; 10735 MW; 2202109E2F3014CD CRC64;
  Last sequence update)
Last annotation update)
   Last sequence update)
Last annotation update)
   Score 25; DB 16;
Pred. No. 9.5e+02;
   98 AA.
  Pred. No. 9.5e
4; Mismatches
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  Created)
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   01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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  01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
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  4; Conservative
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   (TrEMBLrel.
   26 KEFIGKDR 33
   17 AEFISLDN 24
  Nucleoside permease.
  1 XEFIXXDX 8
  1 XEFIXXDX 8
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   Best Local Similarity
Matches 4; Conserv
   Complete proteome. SEQUENCE 97 AA;
  Query Match
Best Local Similarity
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  SEQUENCE FROM N.A.
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   Q8D9R7;
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   08D9R7
  RESULT 40
   Matches
  RESULT 39
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  08D9R7
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklog G.L.G.,
Abril J.F., Agbayani A., An H. J., Anterws-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Barman B.P., Bhandari D., Boaslakov S.,
RA Ballew R.M., Basu A., Berman B.P., Bhandari D., Boaslakov S.,
RA Borkova D., Boctchan M.R., Bouck J., Broketein P., Brottier P.,
R. Borkova D., Botchan M.R., Burler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Durkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C. G., Ferraz, C., Ferraz, G. B.C., Dunn P.,
RA Durbin K.J., Evangelista C. G., Ferraz, C., Ferraz, G. B.C., Dunn P.,
RA Harris N.L., Harvey D., Heinan T.J., Wei M., Glasser K.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heinan T.J., Wei M.-H., Ibegwam C.,
RA Alali M., Kallen F., Karpen G.H., Ke Z., Kennison J.A., Harris M.,
RA Luu X., Mattel B., McIncosh T.C., McLedd M.P., McElenn M.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Markulov G., Milshian N.V., Mobarry C., McLedd M.P., McSherson D.,
RA Merkulov G., Milshian N.V., Mobarry C., Morris J., Moshrefi A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shier B., Spradiling A.C., Standers E., Wang X.,
RA Shier B., Spradiling A.C., Standers E., Wang X.,
RA Shier B., Spradiling A.C., Standers E., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinsten M., Skupski M.P., Smith T.,
RA Wang S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Jenez A.H., Rayen E.W., Rober E.W., Rober E.W., Shong S., Zhon X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Ruber B. C., Siden H., Shier B., Spradiling A.K., Rober B., Shier B., Spradilin
  Gaps
  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
  .,
  Score 25, DB 5, Length 98;
red. No. 9.6e+02;
Mismatches 0; Indels
  STRAIN-CRECON-R; TISSUE-Salivary gland; Wright L.G., Chen T., Thummel C.S., Guild G.M.; Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases. EMBL, AE003530; AAF49591.1;
  11749 MW; 0D769F1A427D2852 CRC64;
  01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
   99 AA.
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  FlyBase; FBgn0014850; Eig71Ej.
InterPro; IPR003475; Insect_Unk.
Pfam; PF02448; L71; 1.
   100.08;
   Phenol hydroxylase component.
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Gaps

Q863N9

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MEDLINE=22423060; PubMed=12534463; Nelson R.J., Hilbert H., Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
                         "Nucleotide sequence of the 3'-terminal region of carnation latent
  MEDLINE=91324119; PubMed=1713905; Meehan B.M., Mills P.R.; "Nucleotide sequence of the 3'-terminal region of carnation latent
  Intervirology 32:262-267(1991).
EMBL; X52627; CAA36855.1; -.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002568; Carla_C4.
   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative nucleic acid binding protein.
Carnation latent virus (CLV).
Viruses, ssRNA positive-strand viruses, no DNA stage; Carlavirus.
   Intervirology 32:262-267(1991).
EMBL; AJ010697; CAA09307.1; -.
GO; GO:0003666; Finucleic acid binding; IEA.
GO; GO:0006555; P:regulation of transcription, DNA-dependent; InterPro; IPR002568; Carla C4.
Ffam; PF01653; Carla C4; 1.
SEQUENCE 102 AA; I1S84 MW; 4574B3FF43B46B19 CRC64;
   0
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   Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
   Length 102;
   Score 25; DB 12; Length 102; Pred. No. 1e+03;
   0; Indels
  Indels
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SEQUENCE 102 AA; 11626 MW; 0474AFBF5FDB1B05 CRC64;
   Last sequence update)
Last annotation update)
  ; Score 25; DB 12;
Pred. No. 1e+03;
4; Mismatches 0;
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  102 AA
   102 AA.
   4; Mismatches
  Transcriptional regulator, Cro/CI family.
   01-070-2003 (TrEMBLrel. 24, Created)
01-070N-2003 (TrEMBLrel. 24, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
  PRT;
   100.0%;
   100.0%;
50.0%; P
   50.0%;
   Query Match
Best Local Similarity 50.00,
-hac 4; Conservative
   4; Conservative
  PRELIMINARY;
  PRELIMINARY;
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90 LEFIGIDL 97
   1 XEFIXXDX 8
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90 LEFIGIDL 97
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  Local Similarity
  SEQUENCE FROM N.A.
  1 XEFIXXDX
  SEQUENCE FROM N.A.
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  QBJJL1
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  Q88LJ6;
  Q88LJ6
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   PP1935
  RESULT 44
  RESULT 45
Q88LJ6
  QBJJLI
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   Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498204; AAP19695.1: -
  Gaps
  benzoate
   Gaps
  Arctonyx collaris.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Melinae,
  Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
  ;
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                         Xu Y., Chen M., Zhang W., Lin M.; "Genetic organization of genes encoding phenol hydroxylase, 1,2-dioxygenase alpha subunit and its regulatory proteins in Curr. Microbiol. 46:235-240(2003). "EMBL; AJS64846; CAD92311.1;
  Length 99;
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50.0%; Pred. No. 9.7e+02;
iive 4; Mismatches 0; Indels
  ; Score 25; DB 6; Length 10
Pred. No. 9.9e+02;
4; Mismatches 0; Indels
   Meehan B.M.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
  101
101 AA; 11428 MW; AD696CB6E0EBD7AC CRC64;
  99 AA; 11542 MW; 11BF76425EA2D847 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
  Last sequence update)
Last annotation update)
   101 AA
   102 AA.
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MEDLINE=22617848; PubMed=12732969;
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SEQUENCE FROM N.A.
MEDLINE=91324119; PubMed=1713905;
Meehan B.M., Mills P.R.;
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  Carnation latent virus (CLV)
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25 AEFIEFDF 32
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VEFIELDI 35
   1 XEFIXXDX 8
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Matches 4; Conserv
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SEQUENCE
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  RESULT 42
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Gaps

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Gaps

RA RA RA RA RI RI DR DR DR SQ

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us-09-660-302e-1.rspt

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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
   SEQUENCE FROM N.A.

Koepfli K.-P., Wayne R.K.;

"Type-1 STS Markers Are More Informative Than Cytochrome b in

"Type-1 STS Markers Are More Informative Than Cytochrome b in

Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
  Eira barbara (Tayra).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
  Hypothetical protein.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Ammmalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
  .
0
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105 105
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Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
growth hormone receptor (Fragment).
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  Syst. Biol. 0:0-0(2003).
EMBL, AF498199; AAP19690.1; -.
GO, GO:0004872; F:receptor activity; IEA.
                         Syst. Biol. 0:0-0(2003).
EMBL; AF498187; AAP19678.1; -.
GO; GO:0004872; F:receptor activity; IEA.
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=22354683; PubMed=12466851;
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50.0%; E
   23,
23,
23,
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   01-MAR-2003 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
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  PRELIMINARY;
  32 VEFIELDI 39
  :|||::||
32 VEFIELDI 39
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MEDLINE=20051044; PubMed=10803899;

MEDLINE=20051044; PubMed=10803899;

Ohdan K., Kuriki T., Takata H., Okada S.;

"Cloning of the cyclodextrin glucanotransferase gene from alkalophilic
"Cloning of the cyclodextrin glucanotransferase gene from alkalophilic
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Appl. Microbiol. Biotechnol. 53:430-44(2000).

EMBL; AB015670; BAA31532.1; - Commander Const.
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  Lontra canadensis (River otter) (Lutra canadensia).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                  Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A., Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Krewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
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   100.0%; Score 25; DB 16; Length 102; 50.0%; Pred. No. 1e+03; Live 4; Mismatches 0; Indels
   Score 25; DB 2; Length 105; Pred. No. 1e+03;
   "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Embricon. Microbiol. 4:799-808(2002).

EMBL; AGD16781; AAN67552.1; -
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01-NOV-1998 (TrEMBLrel. 08, Le
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A2-5a orf4.
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34 VEFIELDI 41
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  Koepfli K.-P., Wayne R.K.,
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).",
Syst. Biol. 0:0-0(2003).
EMBL, AF498190; AAP19681.1;
GO; GO:0004872; F:receptor activity; IEA.
   Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Lutrinae,
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60,770 full-length cDNAs.";
Nature 420.563-573 (2002).
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Hypochhetical protein.
SEQUENCE 105 AA; 12193 MW;
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  Nobell K.-P., Wayne R.K.;
Nobell X.-B., Warkers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustellidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF499184; AAP19675.1;
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   Koepfli K.-P., Wayne R.K.,
"Typel STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustellidae (Mammalia: Carnivora).",
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34 VEFIELDI 41
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  Koepfil K.-P., Wayne R.K.;
Koepfil K. B. Warkers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498188; AAP19579.1; -...
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KOEDILI K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
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  Koepfil K.-P., Wayne R.K.;
Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498192; AAP19683.1; -.
EMBL; AF498192; F:receptor activity; IEA.
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  Koepfil K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
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  107 AA; 12166 MW; 9113E146451EA8BB CRC64;
107 107
107 AA; 12180 MW; 9113E140F3C5C3BB CRC64;
  Q863Q1;
01-UJN-2003 (TrEMBLrel. 24, Created)
01-UJN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
  50.0%; Pred. No. 1e+03; tive 4; Mismatches
   107 AA.
   107 AA.
   Pteronura brasiliensis (Giant otter).
   Growth hormone receptor (Fragment).
   PRT;
   100.0%;
50.0%; E
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Gaps

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Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora)."; Syst. Biol. 0:0-0(2003).
EMBL: AF498195; AAP19686.1; -.
   Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498196; AAP19687.1;
GO:0004872; F:receptor activity; IEA.
  Mustela vison (American mink).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Rissipedia; Mustelidae; Mustelinae;
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Mustellnae,
                                     100.0%; Score 25; DB 6; Length 107; 50.0%; Pred. No. 1e+03;
  Score 25; DB 6; Length 107;
  107 107
107 AA; 12149 MW; 96CCE146450149FE CRC64;
  107 107
107 AA; 12172 MW; 96DBD14658B649FE CRC64;
   01-0TM-2003 (TrEMBLrel. 24, Created)
01-0TM-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
  01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Growth hormone receptor (Fragment).
  ;
  Pred. No. 1e+03;
   107 AA
   Pred. No. 1e+0
4; Mismatches
  107 AA.
  4; Mismatches
  PRT;
  01-JUN-2003 (TrEMBLrel. 24, Created)
   PRT;
   Martes americana (American marten).
  100.08;
  50.08;
                 Query Match
Best Local Similarity 50.00
  PRELIMINARY;
   4; Conservative
   PRELIMINARY;
   34 VEFIELDI 41
  1 XEFIXXDX 8
   :|||::|:
34 VEFIELDI 41
   1 XEFIXXDX 8
   Query Match
Best Local Similarity
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   NCBI_TaxID=9667;
  NCBI_TaxID=9660;
   Receptor.
NON_TER
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  Receptor.
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  Q863P8
   Q863P7;
  Martes.
   Q863P7
   RESULT 60
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  Q863P8
   Q863P7
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  Koepfii K.-P., Wayne R.K.,
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).",
Syst. Biol. 0:0-0(2003).
EMBL; AF498193; AAP19684.1;
GO; GO:0004872; F:receptor activity, IEA.
   Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
  Gaps
  Gaps
  Mustela erminea (Ermine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
   Mustela frenata (Long-tailed weasel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Mustelinae,
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   Score 25; DB 6; Length 107; Pred. No. 1e+03;
   6; Length 107;
   Indels
  0; Indels
  12137 MW; 96DBCA309E7789FE CRC64;
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107 AA; 12140 MW; 96DBD146450149FE CRC64;
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   0;
  100.0%; Score 25; DB 6;
50.0%; Pred. No. 1e+03;
tive 4; Mismatches
   107 AA
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  Syst. Biol. 0:0-0(2003).
EMBL, AF498194; AAP19685.1; -...
GO; GO:0004872; F:receptor activity; IEA.
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   01-0UN-2003 (TrEMBLrel. 24, Created 01-0UN-2003 (TrEMBLrel. 24, Last se 01-0CT-2003 (TrEMBLrel. 25, Last an Growth hormone receptor (Fragment).
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   Growth hormone receptor (Fragment).
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  01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
   4; Conservative
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   Best Local Similarity 50.0 Matches 4; Conservative
   PRELIMINARY;
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34 VEFIELDI 41
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VEFIELDI 41
  107 AA;
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   SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
  NCBI_TaxID=36723;
  NCBI_TaxID=55048;
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  Query Match
   Mustela.
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   Q863P9
   RESULT 59
0863P9
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Koepfii K.-P., Wayne R.K.;

Type-1 STS Markers Are More Informative Than Cytochrome b in

Type-1 STS Markers Are More Informative Than Cytochrome b in

Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";

Syst. Biol. 0.0-0(2003)

EMBL; AR498201; AAP19692.1;

GO, GO:0004872; F:receptor activity; IEA.
   SEQUENCE FROM N.A.

KROPF[II K.-P., Wayne R.K.;
Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustellidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0[203].
EMBL, AF4982200, AAP19691.1; -.
60, GO:0004872; F:receptor activity; IEA.
   Ictonyx striatus (striped polecat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
  6; Length 107;
                    0; Indels
   12140 MW; 96DBD146450149FE CRC64;
  1
107 107
107 AA; 12109 MW; 4048E64F61DBF52C CRC64;
   Q863P2;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
   0
   100.0%; Score 25; DB 6; 50.0%; Pred. No. 1e+03;
  100.0%; Score 25; DB 6;
50.0%; Pred. No. 1e+03;
tive 4; Mismatches
   107 AA
  107 AA
Pred. No. 1e+(
; Mismatches
  PRT;
  50.0%;
   4; Conservative
  PRELIMINARY;
                          4; Conservative
  PRELIMINARY;
   107
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34 VEFIELDI 41
   107 1
107 AA;
  :|||::|:
34 VEFIELDI 41
  1 XEFIXXDX 8
   Query Match
Best Local Similarity
   1 XEFIXXDX 8
   Best Local Similarity
Matches 4; Conserv
  SEQUENCE FROM N.A.
     Best Local Similarity
  NCBI TaxID=204265;
  NCBI_TaxID=55050;
   Galictis vittata.
  Receptor.
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  Receptor.
  SEQUENCE
  Query Match
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   Q863P3
  RESULT 65
Q863P2
   RESULT 64
                               Matches
   Q863P3
   SECOND SE
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  Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498198; AAP19689.1;
GO; GO:0004872; F:receptor activity; IEA.
  Koepfil K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora)."; Syst. Biol. 0:0-0(2003).
EMBL; AF498137; AAP1968811; -.
GO; GO:0004872; F:receptor activity; IEA.
  Gaps
   Gaps
   Gulo gulo (Wolverine) (Gluton).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivoxa, Fissipedia, Mustelidae, Mustelinae,
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
   ..
0
   ..
   Length 107;
  h Similarity 50.0%; Score 25; DB 6; Length 107; 4; Conservative 4; Mismatches 0; Indels
          Score 25; DB 6; Length 107; Pred. No. 1e+03; 4; Mismatches 0; Indels
  96DBD146450149FE CRC64;
  107 AA; 12136 MW; 830606D83B0149FE CRC64;
   24, Last sequence update) 25, Last annotation update)
  Last sequence update)
Last annotation update)
   DB 6;
   107 AA
   Score 25;
   Created)
   Created)
  01-OCT-2003 (TrEMBLrel. 25, Last ar Growth hormone receptor (Fragment).
  PRT;
   Growth hormone receptor (Fragment)
   107 AA; 12140 MW;
  100.08;
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50.0%; E
  01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
  01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
     Query Match
Best Local Similarity 50.0°
4; Conservative
   PRELIMINARY;
  (TrEMBLrel.
   Martes pennanti (Marten)
  PRELIMINARY;
   107
  107
   : | | | : : | : 34 VEFIELDI 41
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34 VEFIELDI 41
   1 XEFIXXDX 8
   1 XEFIXXDX 8
   Local Similarity
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  101
   NCBI_TaxID=48420;
   NCBI_TaxID=76720;
  107
  Receptor.
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  Receptor.
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   Query Match
  SEQUENCE
  Query Match
  Q863P5;
   Q863P5
  Q863P6;
  Martes
  0863P6
   Matches
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RESULT 63

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Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora)."; Syst. Biol. 0:0-0(2003).
EMBL; AF488205; AAP19696.1; -. GO; 60:004872; F:receptor activity; IEA.
  SEQUENCE FROM N.A.

Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
  Gaps
   Bassariscus astutus (ringtail).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Procyonidae; Bassariscus.
   Gaps
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Melinae,
  0;
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   100.0%; Score 25; DB 6; Length 107; 50.0%; Pred. No. 1e+03; tive 4; Mismatches 0; Indels
   100.0%; Score 25; DB 6; Length 107; 50.0%; Pred. No. 1e+03; cive 4; Mismatches 0; Indels
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107 107
107 AA; 12141 MW; C671DBEC450C29F3 CRC64;
  107 AA; 12055 MW; 977B2547E01459BA CRC64;
  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment)
  01-0TN-2003 (TrEMBLrel. 24, Created)
01-0TN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
  107 AA
  107 AA.
   GO; GO:0004872; F:receptor activity; IEA
  Growth hormone receptor (Fragment).
  PRT;
  Syst. Biol. 0:0-0(2003).
EMBL; AF498206; AAP19697.1;
   PRELIMINARY;
   Conservative
  PRELIMINARY;
   4; Conservative
   107
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34 VEFIELDI 41
            1 XEFIXXDX 8
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34 VEFIELDI 41
  1 XEFIXXDX 8
   NCBI_TaxID=204267;
  1 XEFIXXDX 8
   Melogale moschata.
   Local Similarity
  SEQUENCE FROM N.A.
   Local Similarity
  NCBI_TaxID=55047;
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  Melogale
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  Query Match
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  Koepfil K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora)."; Syst. Biol. 0:0-0(2003).
EMBL: AF498202; AAP19693.1; -...
  Meles meles (Eurasian badger).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae; Meles.
  Koepfil K.-P., Wayne R.K.,
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL: AF498203; AAP19694.1;
GO, GO:0004872; F:receptor activity, IEA.
        Gaps
   Gaps
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   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Taxidiinae,
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   100.0%; Score 25; DB 6; Length 107; 50.0%; Pred. No. 1e+03; 0; Indels ive 4; Mismatches 0; Indels
  100.0%; Score 25; DB 6; Length 107; 50.0%; Pred. No. 1e+03; tive 4; Mismatches 0; Indels
      Indels
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107
107 AA; 12110 MW; 96DBD15D44B149FE CRC64;
   12113 MW; 825D0A3F750149FE CRC64;
   Created)
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  01-JUN-2003 (TrEMBLrel. 24, Created 01-JUN-2003 (TrEMBLrel. 24, Last se 01-OCT-2003 (TrEMBLrel. 25, Last an Growth hormone receptor (Fragment).
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  Growth hormone receptor
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VEFIELDI 41
                            1 XEFIXXDX 8
   1 XEFIXXDX 8
   Local Similarity
   SEQUENCE FROM N.A.
  107 AA;
   Best Local Similarity
Matches 4; Conserv
   SEQUENCE FROM N.A.
  NCBI_TaxID=30554;
  NCBI_TaxID=9662;
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   01-JUN-2003
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01-OCT-2003
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   Query Match
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   Q863P1
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  Koepfil K.-P., Wayne R.K.,
"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
BMB., AR498207; AAP19698.1;
GO; GO:0004872; F:receptor activity; IEA.
   SEQUENCE FROM N.A.
STRAIN=UA159 / ATCC 700610 / Serotype C;
MEDLINE=2228563; PubMed=12397186;
Addic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UA159, a cariogenic dental
  Gaps
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   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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  Froc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
EMBL. ABG14982; AANS158.1; -.
Hypothetical protein: Complete proteome.
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107
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Growth hormone receptor (Fragment).
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20 DEFIGYDR 27
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   34 VEFIELDI 41
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A., Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G., Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium Helicobacter hepaticus.";
Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
   Bacteria; Proteôbacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
   Salamoubat M., Genin S., Artiquenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siquier P., Thebault P., Whalen M., Wincker P., Levy M., Wilsenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum.";
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable phage HK022 GP9-related protein.
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Last annotation update)
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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  Zehr J.P., Jenkins B.D., Short S.M., Steward G.F.;
"Nitrogenase gene diversity and microbial community structure: a cross-system comparison.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY223946; AA067605.1;
EMBL; AY223946; AA067611.1;
GO; GO:0005524; F.AF. Phinding; IEA.
GO; GO:0005524; F.AF. Phinding; IEA.
GO; GO:0006118; P:electron transport; IEA.
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Currie J., Collura K.;
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01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
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Last seguence update)
Last annotation update)
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NADH ubiquinone oxidoreductase subunit.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids,
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  STRAIN-cv. Columbia, Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D. Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M., Rabidopsis thaliana chromosome III BAC 717B22 genomic sequence." Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
   0
  Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; Full-length messenger RNA sequences greatly improve genome annotation."
Genome Biol. 0:0-0(2002).
   SECUENCE FROM N.A. Chen H., Johnson-Hopson C., Khan S., Shinn Ecker J.; "Full length cDNA sequence of Arabidopsis thaliana."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
   . Score 25; DB 10; Length 110;
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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STRAIN=IL1403;
MEDLINE=21235186; PubMed=11337471;
MEDLINE=21235186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malaxme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
"The complete genome laguer."
   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
  MEDLINE=21113149; PubMed=11160885; Chopin A., Chopin A., Sorokin A., Ehrlich S.D., Chopin M.-C.; Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin A., Hallysis of eix prophages in Lactococcus lactis IL1403: different genetic structure of temperate and virulent phage populations."; Nucleic Acids Res. 29:644-651(2001).
  no RNA stage; Caudovirales; Siphoviridae.
  SEQUENCE FROM N.A.
Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.,
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF323669; AAR08317.1; -.
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4; Mismatches
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Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

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Anglerty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Angles M.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,

Redmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

Anover D.L., Lindler L.B., Halling S.M., Boyle S.M., Fraser C.M.;

The Brucella suis genome reveals fundamental similarities between

The Brucella suis genome reveals fundamental similarities between

The Brucella suis Anvigoses and symbionts.";

Rembi, Acold; -.

Remple Remover D.L., Complete proteome.

Remple Protein; Complete proteome.

SQ SEQUENCE 110 AA, 11720 MW; 0862D9576C16EF33 CRC64;
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  Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
Cheuk R., Chen H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
A Ishida J., Jones T., Kamiya A., Karlin-Nemmann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nayusen M., Onodera C.S.,
Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
A Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
A Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
C. Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AR725039; AAF26117.1;
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            Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Feldmann K.; "Full-Length cDNA from Arabidopsis thaliana."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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   Nakamura Y., "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC
  Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Muzata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
  Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
   Gaps
  STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
  Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
   STRAIN-Columbia;
Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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DNA Res. 7:131-135(2000).
EMBL; AB024036; BAB02814.1; -.
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FMIL; AB 13512 MW; 81A9D45FFF0B9DC4 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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Last annotation update)
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MEDLINE=20277480; PubMed=10819329;
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MEDLINE=21156231; PubMed=11258796;
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   01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20.
PRELIMINARY;
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Diffreshe A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M., Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F., Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., Wolf Y.I., Hess W.R., "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome.", Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).

EMBL, AE017164; AAQ00101.1; -. Complete proteome.

SEQUENCE 116 AA; 13144 MW; 150B1F4122111 CRC64;
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MEDLINE=22508414:
Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple B.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
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  Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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Bacillus anthracis (strain Ames).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Last annotation update)
   24, Created)
24, Last sequence update)
25, Last annotation update)
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RA RA RA RA RA RT RT DR DR SQ

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STRAIN=El Tor N16961 / Serotype 01;

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Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Bodson R.J., Haft D.H., Hokey E.K., Peterson J.D., Umayam L.A.,

GILL S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragori J., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
   SEQUENCE FROM N.A.
MEDLINE=22336326; PubMed=12446551;
Cheng Y.Q., Tang G.L., Shen B.;
"Identification and Localization of the Gene Cluster Encoding
Biosynthesis of the Antitumor Macrolactam Leinamycin in Streptomyces
   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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   Streptomyces atroolivaceus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Pred. No. 1.2e+03;
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        Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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J. Bacteriol. 184:7013-7024(2002).
J. Facteriol. 184:7013-7024 (2002).
Hypothetical protein.
SEQUENCE. 120 AA; 14105 MW; 95BC6B553E2940D1 CRC64;
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Nature 406:477-483(2000)
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   RESULT 87
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  MEDINB=22668415; PubMed=12721630; Ivanova N., Candelon B., Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhatlacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walumas T., Carchkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N.;
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  DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C., Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.
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  "Genome sequence of Bacillus cereus and comparative analysis with
   "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
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Bacteria, Firmicutes, Bacillales; Bacillaceae; Bacillus
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InterPro; IPR006542; Cons_hypoth1655.
ITIGREAMS; TIGR01655; yeah_fam; 1.
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Q811W3

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Gaps

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RESULT 86

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DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N., Overbeek R.;

"The genome sequence of the facultative intracellular pathogen

Brucella melitensis.";

Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
  MEDLINE=MR-1;
MEDLINE=22297686; PubMed=12368813;
MEDLINE=22297686; PubMed=12368813;
Metadelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Rad T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vanathevan J., Weldman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium
   Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
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  Q8YEY2;
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Matches
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   QBEH18
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  ó.
   Sasaki Y., Ishikawa U., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshimo C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
"Mucled Acids Res. 30:2293-5300(2002).
"BMBL, AP004170; BAC43825.1;
"GO, GO:0006152; P:metabolism; IEA.
  STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE=21359325; PubMed=11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubots J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.M., Koonin B.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
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  Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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01-OCT-2003
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097E59

Matches

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AC 09725
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DC Clost
CC C

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Gaps

0

Biotechnol. 20:1118-1123(2002).

Matches

EMBL; AE015584; AAN54478.1; -.

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Wing R.A., Yu Y., Yang T.J., Nah G., Soderlund C., Chen M., Kim H.-R., Rambo T., Saski C., Henry D., Oates R., Simmons J.;
"Rice Genomic Sequence.";
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MEDLINE=21145866; PubMed=11248100;
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MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006157; AAK03255.1;
InterPro: IPR00520; Cons. hypoth156.
Fram; PF04076; DUF388; 1.
Hypothetical protein; Complete protecome.
SEQUENCE 124 AA; 13402 MW; 289E9736A09BBAA4 CRC64;
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EMBL; AC116600; AAN04141.1; -
EMBL; AC098696; AAN04101.1; -
EMBL; AE017059; AAN052255.1; -.
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SECUENCE.O. Sativa (japonica cultivar-group); STRAIN-cv. Nipponbare;
SPECIES-O.sativa (japonica cultivar-group); STRAIN-cv. Nipponbare;
The Chromosome 10 Sequencing Consortium;
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Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Pasteurella,
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Hypothetical protein.
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  Science 300:1566-1569(2003)
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  STRAIN-Highway;
MEDLINE-2142264; PubMed=11587856;
Barbet A.F., Whitmire W.M., Kamper S.M., Simbi B.H., Ganta R.R.,
Moreland A.L., Mwangi D.M., McGuire T.C., Mahan S.M.;
A subset of Cowdria ruminantium genes important for immune
recognition and protection.";
Gene 275:287-298(2001).
BMBL; AR308662; AAL08808.1;
GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
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InterPro; IPR000051; SAM_bind.
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OSJNAA0036D19.9 OR OSJNBA0050E08.2.
Oryza sativa (Rice), and
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bormatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
  .
0
   ;
0
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Anaplasmataceae; Ehrlichia.
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01-DTN-2003 (TrEMBLrel. 24, Last annotation update)
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J. Virol. 68:2746-2751(1994).
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Yanez R.J., Rodriguez J.R., Nogal M.L., Yuste L., Enriquez C.,
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Of Thogoto virus (Orthomyxoviridae).";
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF493143; AAO73158.1;
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   Gonzalez A., Calvo V., Almazan F., Almendral J.M., Ramirez J.C.,
La Vega I., Blasco R., Vinuela E.,
"Multigene families in African swine fever virus: family 360.";
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"Multigene families in African swine fever virus: family 110.";
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Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus.
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Yanez R.J., Boursnell M., Nogal M.L., Yuste L., Vinuela B.;
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homology with the two largest subunits of DNA-dependent RNA
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MEDLINE=90357780; PubMed=2389555;
Blasco R., Lopez-Otin C., Munoz M., Bockamp B.O., Simon-Mateo C.,
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Almazan F., Murguia J.R., Rodriguez J.M., La Vega I., V. Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
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Lee H.J., Essani K., Smith G.L.;
"The genome sequence of Yaba-like disease virus, a yatapoxvirus.";
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  STRAIN=BA71V;
MEDLINE=94091056; PubMed=8266720;
MEDLINE=94091056; PubMed=826720;
Ferje J.M., Lain S., Vinuela E., Lopez-Otin C.;
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  Hypogeomys antimena (Malagasy giant rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Nesomylnae;
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Thesis (2000), Sir William Dunn School of Pathology, University
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   exogenous antigen via M. . ., IEA.
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"Major histocompatibility complex (MHC) class II polymorphism and paternity in the monogamous Hypogeomys antimena, the endangered, a paternity in the monogamous Hypogeomys antimena, the endangered, largest endemic Malagasy rodent.";

Mol. Ecol. 8:1259-1277(1999).

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P Fam; PF00993; MHC II alpha; I.

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R MART; SM00407; IGGI: II ransmembrane.

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Bisum sativum (Garden pea).
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Fathimani K., Hull K., Harvey S.;
"Sequence analysis of the intracellular domain of rodent growth hormone receptor cDNAS.";
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